



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 179839

TO: Stephen Kapushoc
Location: REM/3A60/2C70
Art Unit: 1634
Wednesday, February 22, 2006
Case Serial Number: 10/785981

From: Barb O'Bryen
Location: Biotech-Chem Library
Remsen 1a69
Phone: 571-272-2518
BBOB
barbara.obryen@uspto.gov

Search Notes

*Swire CIP
requested working folder
2-23-06*

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STIC-Biotech/ChemLib

199839

From: Kapushoc, Stephen T.
Sent: Thursday, February 16, 2006 4:32 PM
To: STIC-Biotech/ChemLib
Subject: Sequence search for 10/785,981

Please search SEQ ID NOs: 1, 2, 3, 4, 5 for application 10/785,981

Thanks,
Steve

Stephen Kapushoc
Art Unit 1634 - USPTO
Tel: 571-272-3312
Office: REM 3A60
Mailbox: REM 2C70

RECEIVED

FEB 16 2006

(STIC)

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA#: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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OM nucleic - nucleic search, using sw model

Run on: February 20, 2006, 10:36:14 ; Search time 3992,58 Seconds

Title: US-10-785-981-1

Perfect score: 660

Sequence: 1 gagaccgaaatactatgt.....tgccacatgaaatggatggat 660

Scoring table: IDENTITY_NUC Gapext 1.0

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0\$ Maximum Match 100\$

Listing first 45 summaries

Database : GenBmbl:
1: gb_ba: *
2: gb_n: *
3: gb_env: *
4: gb_om: *
5: gb_nv: *
6: gb_Dat: *
7: gb_ph: *
8: gb_Dr: *
9: gb_ro: *
10: gb_sts: *
11: gb_sy: *
12: gb_un: *
13: gb_vl: *
14: gb_htg: *
15: gb_pl: *

19 626.4 94.9 1771 9 BC063162
20 626.4 94.9 1775 9 BC072542
21 626.4 94.9 182416 9 AC095724
AC124512 Mus muscu
AC136572 Rattus no
AC102040 Mus muscu
AC166149 Mus muscu
AC166748 Mus muscu
AC110913 Mus muscu
AC13661 Mouse mRNA
AC154274 Mus muscu
AC10339 Rat elongat
AC145861 Pan trogl
AC147556 Mus muscu
AC134666 Mus muscu
AC161170 Mus muscu
AC100406 Mus muscu
AC154479 Mus muscu
D00522 Crictetus
X62245 O. cuniculus
J09823 Octotolagus
AC094797 Rattus no
AC134118 Rattus no
AC116224 Rattus no
AC154254 Mus muscu
AC154774 Mus muscu
AC127720 Rattus no

ALIGNMENTS

RESULT 1

BC004067

LOCUS

DEFINITION

mRNA (cDNA clone

MGC:3590965)

, complete cds.

ACCESSION

BC004067

VERSION

GI:13278545

KEYWORDS

MGC.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 1588)

AUTHORS

Straubinger,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,

Klauber,R.D.,

Collins,F.S.,

Wagner,L.,

Shemesh,C.M.,

Schuler,G.D.,

Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,

Hopkins,R.F.,

Jordan,H.,

Moore,T.,

Max,S.I.,

Wang,J.,

Heih,F.,

Diatchenko,L.,

Marusina,K.,

Farmer,A.A.,

Rubin,G.M.,

Hong,L.,

Stapleton,M.,

Soares,M.B.,

Bonaldo,M.F.,

Casavant,T.L.,

Scheetz,T.E.,

Brownstein,M.J.,

Usdin,T.B.,

Toshiyuki,S.,

Peters,G.J.,

McEwan,P.J.,

Abramson,R.D.,

Malek,J.A.,

Gunnarsson,P.H.,

Richards,S.,

Worley,K.C.,

Hale,S.,

Garcia,A.M.,

Gay,L.J.,

Hulyk,S.W.,

Villain,D.K.,

Muzyk,D.M.,

Sodergran,E.J.,

Lu,X.,

Gibbs,R.A.,

Fahey,J.,

Helton,E.,

Kettman,M.,

Madan,A.,

Rodrigues,S.,

Sanchez,A.,

Whiting,M.,

Madan,A.,

Young,A.C.,

Shevchenko,Y.,

Bouffard,G.G.,

Blakesley,R.W.,

Touchman,J.W.,

Green,E.D.,

Dickson,M.C.,

Rodriguez,A.C.,

Grimwood,J.,

Schmitz,J.,

Meyers,R.M.,

Butterfield,Y.S.,

Krzewinski,M.I.I.,

Skalska,U.,

Smailus,D.E.,

Schnerch,A.,

Schein,J.E.,

Jones,S.J.,

and Marrs,M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

2 (bases 1 to 1588)

Director MGC Project.

Direct Submission

Submitted (28-FEB-2001) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	650	100.0	1588	9	BC004067	Mus muscu	BC004067 Mus muscu
2	650	100.0	1754	9	BC005660	Mus muscu	BC005660 Mus muscu
3	650	100.0	1761	9	BC018485	Mus muscu	BC018485 Mus muscu
4	650	100.0	1771	9	BC092053	Mus muscu	BC092053 Mus muscu
5	650	100.0	1778	9	BC018223	Mus muscu	BC018223 Mus muscu
6	658.4	99.8	1736	9	BC004005	Mus muscu	BC004005 Mus muscu
7	658.4	99.8	1756	9	BC092276	Mus muscu	BC092276 Mus muscu
8	656.8	99.5	1760	9	BC095365	Mus muscu	BC095365 Mus muscu
9	656.8	99.5	1779	9	BC03069	Mus muscu	BC03069 Mus muscu
10	653.6	99.0	181014	9	AL840626	Mouse DNA	AL840626 Mouse DNA
11	647.2	98.1	1722	6	AX306117	Sequence	AX306117 Sequence
12	647.2	98.1	1722	9	MUSEFTU	-	M22432 Mus muscu
C 13	629.6	95.4	145253	9	AC138173	Mus muscu	AC138173 Mus muscu
C 14	629.6	95.4	186564	9	AC119816	Mus muscu	AC119816 Mus muscu
C 15	628.2	95.2	214658	9	AC135059	R. norvegicus	X63361 R. norvegicus
C 16	626.4	94.9	1714	9	RNEFLIAA	-	X61443 R. norvegicus
C 17	626.4	94.9	1737	9	RNEFLAA	-	BC091297 Rattus no

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	650	100.0	1588	9	BC004067	Mus muscu	BC004067 Mus muscu
2	650	100.0	1754	9	BC005660	Mus muscu	BC005660 Mus muscu
3	650	100.0	1761	9	BC018485	Mus muscu	BC018485 Mus muscu
4	650	100.0	1771	9	BC092053	Mus muscu	BC092053 Mus muscu
5	650	100.0	1778	9	BC018223	Mus muscu	BC018223 Mus muscu
6	658.4	99.8	1736	9	BC004005	Mus muscu	BC004005 Mus muscu
7	658.4	99.8	1756	9	BC092276	Mus muscu	BC092276 Mus muscu
8	656.8	99.5	1760	9	BC095365	Mus muscu	BC095365 Mus muscu
9	656.8	99.5	1779	9	BC03069	Mus muscu	BC03069 Mus muscu
10	653.6	99.0	181014	9	AL840626	Mouse DNA	AL840626 Mouse DNA
11	647.2	98.1	1722	6	AX306117	Sequence	AX306117 Sequence
12	647.2	98.1	1722	9	MUSEFTU	-	M22432 Mus muscu
C 13	629.6	95.4	145253	9	AC138173	Mus muscu	AC138173 Mus muscu
C 14	629.6	95.4	186564	9	AC119816	Mus muscu	AC119816 Mus muscu
C 15	628.2	95.2	214658	9	AC135059	R. norvegicus	X63361 R. norvegicus
C 16	626.4	94.9	1714	9	RNEFLIAA	-	X61443 R. norvegicus
C 17	626.4	94.9	1737	9	RNEFLAA	-	BC091297 Rattus no

PUBLISHED

1247932

2 (bases 1 to 1588)

REFERENCE

Directors MGC Project.

Title

Journal

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

2 (bases 1 to 1588)

REFERENCE

Direct Submission

Submitted (28-FEB-2001) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

REMARK
COMMENT
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgbbs-r@mail.nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome
 Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www.shgc.stanford.edu>
 Contact: (Dickson, Mark) mcd@paxil.stanford.edu
 Dickson, M., Schmutz, J., Grimmwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at: <http://image.lnl.gov>. Series: IMAK Plate: 11 Row: C Column: 21 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.

FEATURES

source
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="Czech II"
 /db_xref="taron:10090"
 /clone="MGC:8209 IMAGE:3590965"
 /issue type="Mammary tumor metastasized to lung. Tumor arose spontaneously from a senescent normal mammary (clonal) outgrowth infected with the virus MMTV."
 /clone.lib="NCI CCAP_Mu29"
 /lab_hstr="DBH10B"
 /note="Vector: pCMV-SPORT6"
 1..1588
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 /note="synonyms: MGC18758, MGC27859, MGC7551, MGC8115, MGCS209"
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 /db_xref="GI:13278546"
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 /db_xref="MG:1096881"
 /translation=MGKEKTHNIVVIGHVDSGSKSTTGHLYKCGGLDRTEKFKEPK
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 TTGTSQADCAVLYAGCCEFGISNGOTRBEHALAYTLGKVKLIVNMNDSTEP
 PYSDKRYEBIYKEVSTYIKKGNPDTAVPISGMNDNMPLPSAAMPWFVGKVTR
 KDGSASTGFLLEALDCILUPPTDKPLPQDVYKIGGTVPUVERETSYKPGM
 VTFPAVNPNTTEVKSVNHEALSEALPQDNGFVNQVNSVDVRBNVAGSKNDPP
 MEAAGFTADQVILINHPGQISAGTAFLDCTHJACKPDKRISGKLEDPK
 FLKSGDAAVDPMTYKPGKPMCVESFDYPLPGRPAVRDRQTVAVGVIKADKAAGAK
 VTKSAQAKAQAK"

gene

RESULT 2
LOCUS BC005660 1754 bp mRNA linear ROD 25-JUL-2005
DEFINITION Mus musculus eukaryotic translation elongation factor 1 alpha 1, mRNA (cDNA clone MGC:8115 IMAGE:3588966), complete cds.
ACCESSION BC005660
VERSION BC005660.1 GI:13542942
KEYWORDS MGC.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Gires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
 Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
 Klausner, R.D., Collins, F.S., Wagner, L., Shemesh, C.M., Schuler, G.D.,
 Altschul, S.P., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
 Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
 Sapegin, P., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Tohjiyuki, S., Carninci, P., Prange, C., Raha, S. S., Loquellano, N. A., Peters, S., G.J., Abramson, R.D., Mullany, S. J., Bosak, S. A., McEwan, P. J., McKernan, R.K., Malek, J.A., Gunaratne, P. H., Richards, S., Worley, K. C., Hale, S., Garcia, A. M., Gay, L. J., Hulyk, S. W., Villalon, D. K., Muzny, D. M., Sodergren, E. J., Lu, X., Gibbs, R. A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A. C., Shevchenko, Y., Boughard, G. G., Blakesley, R. W., Touchman, J. W., Green, E. D., Dickson, M. C., Rodriguez, A. C., Grimwood, J., Schmitz, J., Myers, R. M., Butterfield, Y. S., Krywinski, M. I., Skalska, U., Smailus, D. E., Scherzer, A., Schein, J. E., Jones, S. J., and Marrs, M. A.

Mammalian Gene Collection Program Team
TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBLMED 12477932

CDS

Query Match 100.0%; Score 660; DB 9; Length 1588;
 Best Local Similarity 100.0%; Pred. No. 6..6e-186; Mismatches 0; Indels 0; Gaps 0;
 Matches 660; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GAGACCGAGCATACTATGTGACCATCATGATGCCAGACAGACTCATCAA 60
 Db 298 GAGACCGAGCATACTATGTGACCATCATGATGCCAGACAGACTCATCAA 357
 Qy 61 AACATGATTAAGGGCATCCAGGTGACATTCAGGTGATGTGTTGCTGTT 120
 Db 358 AACATGATTAAGGGCATCCAGGTGACATTCAGGTGATGTGTTGCTGTT 417
 Qy 121 GGTGAATTGAGCTGATCTCCAAAGAACGGCAGACCCGGACATGCTCTGGCT 180

ORIGIN

Qy 1 GAGACCGAGCATACTATGTGACCATCATGATGCCAGACAGACTCATCAA 60
 Db 298 GAGACCGAGCATACTATGTGACCATCATGATGCCAGACAGACTCATCAA 357
 Qy 61 AACATGATTAAGGGCATCCAGGTGACATTCAGGTGATGTGTTGCTGTT 120
 Db 358 AACATGATTAAGGGCATCCAGGTGACATTCAGGTGATGTGTTGCTGTT 417
 Qy 121 GGTGAATTGAGCTGATCTCCAAAGAACGGCAGACCCGGACATGCTCTGGCT 180

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OM nucleic - nucleic search, using sw model

Run on: February 20, 2006, 10:32:49 ; Search time 560.102 Seconds
 (without alignments)

Title: US-10-785-981-1

Perfect score: 660

Sequence: 1 gagaccgaaatactatgt.....tgccacatgaagtttgtagt 660

Scoring table: IDENTITY NUC Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0‡ Maximum Match 100§

Listing first 45 summaries

Database :	N_Geneseq_21:*
1:	Geneseqm1980s:*
2:	Geneseqm1990s:*
3:	Geneseqm2001as:*
4:	Geneseqm2001bs:*
5:	Geneseqm2001bs:*
6:	Geneseqm2002as:*
7:	Geneseqm2002as:*
8:	Geneseqm2003as:*
9:	Geneseqm2003as:*
10:	Geneseqm2003cs:*
11:	Geneseqm2004ds:*
12:	Geneseqm2004as:*
13:	Geneseqm2004bs:*
14:	Geneseqm2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	660	100.0	660	14	AD259038		Adz89038 Pig growth
2	660	100.0	660	14	AD279331		Adz79331 Swine growth
3	660	100.0	660	14	ADZ7168		Adz77168 Pig growth
4	655	2	99.3	1722	10	ADF0645	Adf0645 Rat angio
5	647	2	98.1	1722	6	AB19778	Ab199778 Mouse iSC
6	621	2	94.2	1404	10	ADB58712	Adb58712 Toxicity-
7	621	6	94.2	1404	13	ADV41496	Adv41496 Rat cardi
C	8	581	6	88.1	1246	4	Aai2127 Probe #12
C	9	581	6	88.1	1246	4	Aab67206 Human foie
C	10	581	6	88.1	1246	4	Aai47423 Probe #16
C	11	581	6	88.1	1246	4	Aba49293 Human bre
C	12	581	6	88.1	1246	4	Aba34302 Probe #12
C	13	581	6	88.1	1246	4	Aak41382 Human bon
C	14	581	6	88.1	1246	4	Aak15648 Human bra
C	15	581	6	88.1	1246	4	Abs40975 Human liv
C	16	581	6	88.1	1246	5	Aai07827 Probe #78
C	17	581	6	88.1	1246	6	Abc15387 Human gen
C	18	581	6	88.1	1389	12	Ado00457 Novel hum
C	19	581	6	88.1	1389	12	Adn98888 Novel hum

ALIGNMENTS

RESULT 1	
ID	ADz89038
XX	standard; DNA; 660 BP.
AC	ADz89038;
XX	
DT	28-JUL-2005 (first entry)
XX	
DE	pIg growth factor I (GF I) gene, seq id 1.
XX	
KW	Growth; biochip; swine; hog raising; growth factor I; gene; ds.
XX	
OS	Sus scrofa; Kagoshima Berkshire.
XX	
PN	US2005112597-A1.
XX	
PD	25-MAY-2005.
XX	
PF	26-FEB-2004; 2004US-00785981.
XX	
PR	24-NOV-2003; 2003KR-00083653.
XX	
PA	(KIMC/) KIM C.
PA	(YEONJ/) YEO J.
PA	(LEEJ/) LEE J.
PA	(SONG/) SONG Y.
PA	(CHOK/) CHO K.
PA	(CHUNJ/) CHUNG K.
PA	(KIMI/) KIM I.
PA	(JINS/) JIN S.
PA	(PARK/) PARK S.
PA	(JUNG/) JUNG J.
PA	(LEEJ/) LEE M.
PA	(KWON/) KWON E.
PA	(CHOE/) CHO E.
PA	(CHOH/) CHO H.
PA	(SHIN/) SHIN S.
PA	(NRMH/) NAM H.
PA	(HONG/) HONG Y.
PA	(HONG/) HONG S.
PA	(KANG/) KANG Y.
PA	(HAYY/) HAY Y.

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OM nucleic - nucleic search, using bw model

Run on: February 20, 2006, 10:51:20 ; Search time 3910,41 Seconds
 (without alignments)

Title: US-10-785-981-1
 Perfect score: 660
 Sequence: 1 gagaccgaaatactatgt.....tgcaaccatggaaatgttttgagt 660

Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0*
 Maximum Match 0*
 Listing first 45 summaries

Result No.	Score	Query	Match	Length	DB	ID	Description
1	656.8	gb_gbb1:*	1	100.0	BC092292		BW945443 UI-M-EMO-C
2	656.8	gb_gbb1:*	2	99.5	673	3	CX788670 HESE3_101
3	656.8	gb_gbb1:*	3	99.5	678	8	CB243368 UI-M-FDO-
4	656.8	gb_gbb1:*	4	99.5	710	6	BN945776 UI-M-EMO-B
5	656.8	gb_gbb1:*	5	99.5	719	3	BN946759 UI-M-EMO-
6	656.8	gb_gbb1:*	6	99.5	746	3	BN946759 UI-M-EMO-
7	656.8	gb_gbb1:*	7	99.5	748	3	BN042422 UI-M-EMO-
8	656.8	gb_gbb1:*	8	99.5	749	3	CQ322009 UI-M-FXO-
9	656.8	gb_gbb1:*	9	99.5	755	5	BQ144687 UI-M-ER0-
10	656.8	gb_gbb1:*	10	99.5	757	7	CP951596 UI-M-HLO-
11	656.8	gb_gbb1:*	11	99.5	760	8	CP949906 UI-M-HKO-
12	656.8	gb_gbb1:*	12	99.5	764	3	BQ177933 UI-M-ER0-
13	656.8	gb_gbb1:*	13	99.5	771	3	BQ17724 UI-M-ER0-
14	656.8	gb_gbb1:*	14	99.5	808	5	BQ571059 UI-M-FBO-
15	656.8	gb_gbb1:*	15	99.5	879	5	BUS15595 AGENCOURT
16	656.8	gb_gbb1:*	16	99.5	926	6	CA97421 AGENCOURT
17	656.8	gb_gbb1:*	17	99.5	928	8	BQ922583 AGENCOURT
18	656.8	gb_gbb1:*	18	99.5	1111	3	BH452687 AGENCOURT
19	656.8	gb_gbb1:*	19	99.5	1145	3	BW461263 AGENCOURT
20	656.8	gb_gbb1:*	20	99.5	1153	5	BUS15235 AGENCOURT
21	656.8	gb_gbb1:*	21	99.5	1733	4	AK081725 Mus muscu
22	656.8	gb_gbb1:*	22	99.5	1734	4	AK076696 Mus muscu

ALIGNMENTS

RESULT 1	BC092292	LOCUS	Mus musculus cDNA clone IMAGE:5068840, containing frame-shift errors.	HTC
	BC092292	DEFINITION		
	BC092292	ACCESSION		
	BC092292.1	VERSION		
	GI:62185631	KEYWORDS		
		SOURCE	Mus musculus (house mouse)	
		ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciuromorpha; Murioidea; Muridae; Murinae; Mus .	
		REFERENCE	1 (bases 1 to 1700)	
		AUTHORS	Krausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Schuler,G.D., Altschul,S.F., Zeeberg,B., Bustow,K.H., Schaeter,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.H., Usdin,T.B., Toshimatsu,S., Carninci,P., Prange,C., Raha,S.S., Loqueland,N.A., Peters,G.J., Abramson,R.D., Mulaliy,S.J., Bosak,S.A., McEvans,P.J., McEvans,P.J., Richards,S.,	
			Worley,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hullik,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettman,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,J., Grinwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalaka,U., Smailus,D.E., Schnarreich,A., Schein,J.B., Jones,S.J. and Marra,M.A.	
		CONSRITM	Mammalian Gene Collection Program Team	
		TITLE	Mammalian and initial analysis of more than 15,000 full-length human and mouse cDNA sequences	
		JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)	
		PUBLMED	12477932	
		REFERENCE	2 (bases 1 to 1700)	
		AUTHORS	NHG C Project	
		CONSRITM	Direct Submission	
		TITLE	Submitted (01-APR-2005) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2550, USA	
		JOURNAL	NHG C Project URL: http://mgc.ncbi.nih.gov	
		REMARK	NIH-MGC Project Contact: MGC help desk	
		COMMENT		

Email:	cgapbs-re@mail.nih.gov	Qy	421	GGCAAGTGCAGTGACCAACAGCTGAAAGCTGGATTGATCTTACCCACACTGT	480
Tissue Procurement:	Gilbert Smith, Ph.D.	Db	673	GGCATGTGCAGTGACCAACAGCTGAAAGCTGGATTGATCTTACCCACACTGT	732
CDNA Library Preparation:	Life Technologies, Inc.	Qy	481	CCAACTGACAAGCTCTCGACTGCCCTCAGATGTCATAAATTGGGCTTGGC	540
CDNA Library Arrayed by:	The I.M.A.G.E. Consortium (LILN)	Db	733	CCAACTGACAAGCTCTCGACTGCCCTCAGATGTCATAAATTGGGCTTGGC	792
DNA Sequencing by:	National Institutes of Health Intramural Sequencing Center (NSIC), Gaithersburg, Maryland; Web site: http://www.nisc.nih.gov/	Qy	541	ACTGCTCCCTGCGCCGAGTGGAGACAGCTGGTCTGTTCAACCTGGTCTGTT	600
Akther, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blieske, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dierich, N.L., Granite, S., Guan, X., Gupta, J., Haghghi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Lasic, P., Legaspi, R., Maduro, Q.L., Mastello, C., Maskeri, B., Mastrion, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, R., Thomas, P.J., Touchman, J.W., Surgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.	Db	793	ACTGCTCCCTGCGCCGAGTGGAGACAGCTGGTCTGTTCAACCTGGTCTGTT	852	
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LILN at: http://image.llnl.gov	RESULT 2	Qy	601	GTCAGCTAATGTAACACTGAGTCAGTGTGAATGACATGAAGCTTGAGT	660
SERIAL: TRAK Plate: 193 Row: n Column: 8 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer Frequency ORF analysis, GenomeScan gene prediction, Similarity but not identity to protein, GenoMEScan gene prediction, Similarity but not identity to protein. This clone has the following problem: frame shifted.	BM945443	Db	853	GTCAGCTAATGTAACACTGAGTCAGTGTGAATGACATGAAGCTTGAGT	912
FEATURES source	LOCUS DEFINITION	Qy	673	bpp mRNA linear EST 14-MAR-2002 NIH_BMAP_EM0 Mus musculus cDNA clone IMAGE:5692190 5', mRNA sequence.	673 bp
	ACCESSION	Db	673	BM945443	NIH_BMAP_EM0 Mus musculus cDNA clone IMAGE:5692190 5', mRNA sequence.
	VERSION	Qy	673	BM945443.1 GI:19429028 EST.	BM945443.1 GI:19429028
	KEYWORDS	Db	673	Mus musculus (house mouse)	
	SOURCE	ORGANISM	673	Bukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciuromorphati; Murioidea; Muridae; Murinae; Mus;	Mus musculus
	REFERENCE	Qy	673	National Institute of Health, Mammalian Gene Collection (MGC) Unpublished (1999)	NIH-MGC http://mgc.nci.nih.gov/
	AUTHORS	Db	673	Tissue Procurement: Dr. James Lin, University of Iowa cDNA Library Prepared by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LILN at: http://image.llnl.gov	CONTACT: Robert Strausberg, Ph.D.
	JOURNAL	Qy	673	This clone was contributed by the Brain Molecular Anatomy Project (BMAP)	COMMENT: Email: cgapbs-re@mail.nih.gov
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		/organism="Mus musculus"	673	Organism="Mus musculus"	
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	Matches 660; Conservative	0;	Mismatches 0; Indels 0; Gaps 0;		
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Db	313	AACATGATACAGGCCATCCAGCTGATCGCTGAGCAAGACTCATCAA	372		
Qy	121	GGTGAATTGAGCTGTGATCTCCAGAACGGCGAGCCGGAGCATCTCTCTGGT	180		
Db	373	GGTGAATTGAGCTGTGATCTCCAGAACGGCGAGCCGGAGCATCTCTCTGGT	432		
Qy	181	TACACCTGGTGGTCAAACAAATGGATTCACCGAGCCA	240		
Db	433	TACACCTGGTCAAACAAATGGATTCACCGAGCCA	492		
Qy	241	CCATACAGTCAGAAAGATAAGAGAAATGTGTAAGGAGTCACCATTAAGAA	300		
Db	493	CCATACAGTCAGAAAGATAAGAGAAATGTGTAAGGAGTCACCATTAAGAA	552		
Qy	301	ATGGCTTACACCTGACAGTAGCATTTGTGCCAATTCTGGTGAATGGTACAC	360		
Db	553	ATGGCTTACACCTGACAGTAGCATTTGTGCCAATTCTGGTGAATGGTACAC	612		
Qy	361	ATGCTGGAAAGCTGCTTCAAGGGTGGAAAGTCTCCCGCAAAGT	420		
Db	613	ATGCTGGAAAGCTGCTTCAAGGGTGGAAAGTCTCCCGCAAAGT	672		
		ORIGIN			

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Gencore version 5.1.7

OM nucleic - nucleic search, using sw model.

Run on: February 20, 2006, 11:15:29 ; Search time 161.946 Seconds

(without alignments)
7244.353 Million cell updates/sec

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Perfect score: 660
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Total number of hits satisfying chosen parameters: 2606114

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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	581.6	88.1	1506	3	US-09-023-655-1278	Sequence 1278, App
2	581.6	88.1	1506	3	US-09-949-016-204	Sequence 204, App
3	581.6	88.1	1747	3	US-09-949-016-1833	Sequence 1833, App
4	581.6	88.1	1749	3	US-09-949-016-3699	Sequence 3699, App
5	581.6	88.1	1749	3	US-09-949-016-3700	Sequence 3700, App
6	581.6	88.1	5749	3	US-09-949-016-15441	Sequence 15441, A
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8	580	87.9	1753	9	5225348-2	Patent No. 5225348
9	570.4	86.4	2128	2	US-09-371-377-16	Sequence 16, Appl
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11	562.4	85.2	1750	3	US-09-949-016-2972	Sequence 2972, AP
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13	562.4	85.2	5750	3	US-09-949-016-14714	Sequence 14714, A
14	562.4	85.2	5750	3	US-09-949-016-14715	Sequence 14715, A
c 15	458.4	69.5	546	3	US-09-385-982-466	Sequence 466, APP
c 16	423.4	64.2	1229	3	US-09-655-1068	Sequence 1068, AP
c 17	420.6	63.7	1747	3	US-09-949-016-1948	Sequence 1948, AP
c 18	401.6	60.8	533	3	US-09-328-111-469	Sequence 469, APP
c 19	56.3	56.3	601	3	US-09-949-016-22182	Sequence 22182, A
c 20	371.4	56.3	601	3	US-09-949-016-131604	Sequence 131604,
c 21	371.4	56.3	601	3	US-09-949-016-131608	Sequence 131608,
c 22	363	55.0	85963	3	US-09-949-016-13804	Sequence 13804, A
c 23	340.6	51.6	1377	3	US-09-614-221A-492	Sequence 492, APP
c 24	339	51.4	1500	3	US-09-174-768-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-09-023-655-1278
; Sequence 1278, Application US/09023655

; Patent No. 6607879
GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; ADDRESS: INCYTE PHARMACEUTICALS, INC.
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER:
; TELEPHONE: (650) 855-0555
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1278:
SEQUENCE CHARACTERISTICS:
; LENGTH: 1506 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: 931097

US-09-023-655-1278

Query Match 88.1%; Score 581.6; DB 3; Length 1506;
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 Db 834 ACTGTCCTGTGGCGAGTGGAGACTGGTGTCAACCTGGATGTGGTTACCTT 893
 Qy 601 GCTCCAGTCAATGTAACTGAAGTCAACTGTGTAATGCAACCATGAAGCTTGACT 660
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RESULT 2

US-09-949-016-204
 Sequence 204, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLO01307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1833 LENGTH: 1747

RESULT 3

US-09-949-016-1833
 Sequence 1833, Application US/09949016
 Patent No. 6812339
 GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CLO01307
 CURRENT APPLICATION NUMBER: US/09/949,016
 CURRENT FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 1833 LENGTH: 1747

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25	573.6	86.9	2106	9	US-10-367-057-166	Sequence 166, AppI
26	573.6	86.9	2106	9	US-10-956-157-624	Sequence 624, AppI
27	570.4	86.4	2128	9	US-10-955-119-22	Sequence 22, AppI
28	569.6	86.3	1709	8	US-09-822-613-00723	Sequence 130623, AppI
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33	545.4	82.6	730	7	US-10-085-783A-45065	Sequence 45065, A
34	523	79.2	630	7	US-10-242-535A-37724	Sequence 38724, A
35	523	79.2	630	7	US-10-085-783A-38724	Sequence 38724, A
36	501.8	76.0	1982	3	US-09-864-761-3395	Sequence 1935, AP
37	493.2	74.7	787	6	US-10-264-070-2449	Sequence 2449, AP
38	479.4	72.6	1413	9	US-10-450-763-2989	Sequence 27989, A
39	477.6	72.4	1931	9	US-10-450-763-11410	Sequence 11410, A
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42	467	70.8	1389	9	US-10-450-763-28843	Sequence 26843, A
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ALIGNMENTS

Maximum Match 100%
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RESULT 1
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 ; Sequence 1, Application US/10785981
 ; Publication No. US20050112597A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GYONGSANGNAM-DO
 ; CRAWFORD, KIM
 ; TITLE OF INVENTION: SCREENING EXPRESSION PROFILE OF GROWTH SPECIFIC GENES IN
 ; TISSUE AND FUNCTIONAL CDNA CHIP PREPARED BY USING THE SAME
 ; FILE REFERENCE: 3884-0120P
 ; CURRENT APPLICATION NUMBER: US/10/785,981
 ; CURRENT FILING DATE: 2004-06-26
 ; PRIORITY APPLICATION NUMBER: KR 2003-83653
 ; PRIORITY APPLICATION NUMBER: KR 2003-83653

No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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5	655.2	99.3	1722	6	US-10-3-16-253-208	Sequence 208, App
6	581.6	88.1	1246	3	US-9-864-761-19622	Sequence 19622, A
7	581.6	88.1	1494	8	US-10-416-330-11	Sequence 11, Appli
8	581.6	88.1	1504	7	US-10-611-643-1278	Sequence 1278, Ap
9	581.6	88.1	1696	6	US-10-374-979-74	Sequence 74, Appli
10	581.6	88.1	1696	7	US-10-182-936A-74	Sequence 74, Appli
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13	581.6	88.1	1696	9	US-10-247-173-653	Sequence 653, App
14	581.6	88.1	1720	8	US-10-278-698-242	Sequence 242, App
15	581.6	88.1	1720	8	US-10-278-698-756	Sequence 756, App
16	581.6	88.1	1833	7	US-10-231-956A-76	Sequence 76, Appli
17	581.6	88.1	1833	8	US-10-684-422-254	Sequence 254, App
18	581.6	88.1	1833	9	US-10-489-740-65	Sequence 65, Appli
19	581.6	88.1	1833	9	US-10-95-157-623	Sequence 623, Appli
20	581.6	88.1	1837	7	US-10-93-703-75	Sequence 75, Appli
21	581.6	88.1	1950	3	US-0-864-761-2840	Sequence 2840, Ap
22	581.6	88.1	3415	3	US-0-864-73-245-438	Sequence 38, App
23	578.4	87.6	9559	9	US-10-617-316-38	Sequence 38, App

November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New). Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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Run on:	February 20, 2006, 10:36:14 ; Search time 3205.16 Seconds (without alignments)	CS071067 Sequence
Title:	US-10-785-981-2	W36769 Homo sapien
Perfect score:	530	CQ731011 Sequence
Sequence:	1 gctgtatcgatggggaaatc.....tagtgcattgaaatctgg 530	BC008538 Mus muscu
Scoring table:	IDENTITY_NUC Gapext 1.0	AB059398 Bos tauru
Searched:	5883141 seqs, 28421725653 residues	AB021180 Gallus ga
Total number of hits satisfying chosen parameters:	11766282	BC093082 Homo sapi
Minimum DB seq length:	0	CS018089 Sequence
Maximum DB seq length:	20000000000	AF11784 Homo sapi
Post-processing:	Minimum Match 0% Maximum Match 100%	CQ729334 Sequence
	Listing first 45 summaries	BC025604 Sequence
Database :	GenEmbl: 1: gb_ba: 2: gb_in: 3: gb_env: 4: gb_om: 5: gb_ov: 6: gb_pat: 7: gb_ph: 8: gb_Dr: 9: gb_ro: 10: gb_sts: 11: gb_sy: 12: gb_un: 13: gb_vl: 14: gb_htg: 15: gb_pl: 	CS025604 Sequence
	GenEmbl: 1: gb_ba: 2: gb_in: 3: gb_env: 4: gb_om: 5: gb_ov: 6: gb_pat: 7: gb_ph: 8: gb_Dr: 9: gb_ro: 10: gb_sts: 11: gb_sy: 12: gb_un: 13: gb_vl: 14: gb_htg: 15: gb_pl: 	AF272034 Gallus ga
		AY116217 Gallus ga
		AB088365 Equus cab
		U87231 Gallus gall
		AY116218 Gallus ga
		AF272033 Gallus ga
		AF240689 Rana pipi
		AF240690 Rana pipi
		AX770500 Sequence
		XJ3988 Human mRNA
		AF336977 Mus muscu
		BC044194 Danio rer
		AF211650 Danio rer
		BC076678 Xenopus t
		ALIGMENTS
		RESULT 1
		AB025261 Sub scrofa mRNA for myosin heavy chain 2b, complete cds.
		LOCUS AB025261
		ACCESSION AB025261
		VERSION AB025261.1
		KEYWORDS GI:5360747 myosin heavy chain 2b.
		SOURCE Sub scrofa (pig)
		ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus
		REFERENCE 1 (sites)
		AUTHORS Chikuni K., Tanabe R., Muroya S. and Nakajima I.
		TITLE Differences in molecular structure among the porcine myosin heavy chain 2a, -2x, and -2b isoforms
		JOURNAL Meat Sci 57, 311-317 (2001)
		2 (bases 1 to 5929)
		AUTHORS Chikuni K.
		TITLE Direct Submission
		JOURNAL Submitted (23-MAR-1999) Kochi Chikuni, National Institute of Animal Industry, Meat Science Laboratory;
		Nourin-kenkyu-danchi, P.O.box 5, Tsukuba, Ibaraki 305-0901, Japan
		FEATURES /organism="Sus scrofa" /mol_type="mRNA" /strain="Landrace" /db_xref="Taxon:9823" /sex="male" /tissue_type="skeletal muscle" /dev_stage="adult" /product="myosin heavy chain 2b" /protein_id="BA82144-1" /db_xref="GI: 5360748" /translation="MSDQEAIIFGERAPYLRKSEKEERIEAQNKPDATKTSVFAVPK ESFVKCTVQSREGKVTVKTEAGATLTVKEDQVFNPNPKPKFDKIEDMMTHLHEPV
		source 1. .5929
		Location/Qualifiers
		source /Email:chikuni@nai.affrc.go.jp, Tel: +81-298-38-8686, Fax: +81-298-38-8666
		CDS 54 .5867
		/codon_start=1
		/product="myosin heavy chain 2b"
		/protein_id="BA82144-1"
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		/translation="MSDQEAIIFGERAPYLRKSEKEERIEAQNKPDATKTSVFAVPK ESFVKCTVQSREGKVTVKTEAGATLTVKEDQVFNPNPKPKFDKIEDMMTHLHEPV
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		Result No. Score Query Match Length DB ID Description
- - -	1 530 100.0 AB025261 Sub scrofa	- AB025261 Sub scrof
	2 526.8 99.4 AB025262 Sub scrof	- AB025262 Sub scrof
	3 482 90.9 AB059399 Bos tauru	
	4 477.2 90.0 AB088366 Equus cab	AB088366 Equus cab
	5 470.8 88.8 BC022376 Homo sapi	BC022376 Homo sapi
	6 470.8 88.8 CS018093 Sequence	CS018093 Sequence
	7 470.8 88.8 CS025608 Sequence	CS025608 Sequence
	8 470.8 88.8 CS119311 Sequence	CS119311 Sequence
	9 470.8 88.8 AF11785 Homo sapi	AF11785 Homo sapi
	10 470.8 88.8 CQ731010 Sequence	CQ731010 Sequence
	11 459.6 86.7 OCU2574 Oryctolagus	OCU2574 Oryctolagus
	12 450 84.9 AB025260 Sub scrof	AB025260 Sub scrof
	13 431.2 81.4 AK220548 Mus muscu	AK220548 Mus muscu
	14 424.4 80.1 CR23587 Gallus ga	CR23587 Gallus ga
	15 424.4 80.1 CQ733076 Sequence	CQ733076 Sequence
	16 424.4 80.1 CS018091 Sequence	CS018091 Sequence
	17 424.4 80.1 CS025606 Sequence	CS025606 Sequence
	18 424.4 80.1 AF111783 Homo sapi	AF111783 Homo sapi

LYNLLKERYAAMWILTYSSCEFCUTVNPYKWLPUYNAEVUTTAYRKKERQEAAPPFESISSD
NQYOMLTDRNNSLITGEAGSCKTAKTRVYIPTAVLGEKEEKPFPKGKQH
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TKEEBHHOMLNNSERQKLOPESGEKTRDOLSEVK
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SNAACALUKKQNDKLLAENHKYSETQOALEASQESRSPSTLEPKVUNYQESI
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LEHEBGKLURLQOLELNQVOSKEDURKIAKDEEDOMERKHNTRVTEMOSTLDAEERS
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LKEQUEVRANTNMQELBEHLASLQESTSERQVQDLSQSERVQDLSQSERVQDLSQ
NTKCKLLETDSI SOLOGEMEDIYOPARNABEKAKAITAAMMABEELKEQDTSUHLER
RICHERRVKEVLYQTEDRDNVNLQDLDYDLSQKVRVYKROQAEAEQQRNVYTKL
LQHLEBEAERADIAESQVNKLRYKSVHIVSE"

ORIGIN	Query Match	Best Local Similarity	Matches
		530;	Cons.
Dy	1	GCTGACT	
Db	551	GCTGACT	
Dy	61	TGTGAA	
Db	611	TGTGAA	
Dy	121	GAAGGC	
Db	671	GAAGGC	
Dy	181	CAACCCC	
Db	731	CAACCCC	
Dy	241	CITTTGGG	
Db	791	CITTTGGG	
Dy	301	CGAAAC	
Db	851	CGAAAC	
Dy	361	CCACAT	
Db	911	CCACAT	
Dy	421	CACCAC	
Db	971	CACCAC	
Dy	481	TGATGAC	
Db	1031	TGATGAC	

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OM nucleic - nucleic search, using bw mode]

Run on: February 20, 2006, 10:32:49 ; Search time 449.779 Seconds
(without alignments)
7853.391 Million cell updates/sec

Title: US-10-785-981-2

Perfect score: 530

Sequence: 1 gctgtactgtatcgggagaatc.....taggccattgaaatccgg 530

Scoring table: IDENTITY_NUC
Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :	N_Geneseq_21:*
	1: geneseqn1980s:*
	2: geneseqn1990s:*
	3: geneseqn2001ab:*
	4: geneseqn2001bs:*
	5: geneseqn2002ab:*
	6: geneseqn2002bs:*
	7: geneseqn2003ab:*
	8: geneseqn2003bs:*
	9: geneseqn2003cb:*
	10: geneseqn2003cs:*
	11: geneseqn2003ds:*
	12: geneseqn2004ab:*
	13: geneseqn2004bs:*
	14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	530	100.0	530	14	AD289039		Adz89039 Pig growth
2	530	100.0	530	14	AD279332		Adz79332 Swine growth
3	530	100.0	530	14	AD277169		Adz277169 Pig growth
4	470.8	88.8	5925	10	ADD29577		Add29577 Human tum
5	470.8	88.8	5925	14	ADM95930		Adm95930 cDNA encod
6	470.8	88.8	5925	14	ADX15796		Adx15796 DNA encod
7	470.8	88.8	5925	14	ADX25983		Adx25983 Novel cel
8	432.4	81.6	5874	5	AAS85420		Aas85420 DNA encod
9	424.4	80.1	6016	14	ADM95928		Adm95928 cDNA encod
10	424.4	80.1	6016	14	ADX15794		Adx15794 DNA encod
11	424.4	80.1	6016	14	ADX25985		Adx25985 Novel cel
12	421.6	79.5	6010	12	ADQ22038		Adq22038 Human sof
13	421.6	79.5	6010	12	ADQ22007		Adq22007 Human sof
14	421.6	79.5	6010	12	ADQ17241		Adq17241 Human sof
15	421.6	79.5	6010	12	ADQ17288		Adq17288 Human sof
16	421.6	79.5	6016	4	AAH57390		Aah57390 Human ske
17	421.2	79.5	5595	14	ADX26120		Adx26120 Novel cel
18	411.4	78.6	5956	14	ADM95926		Adm95926 cDNA encod
19	416.4	78.6	6085	14	ADX15792		Adx15792 DNA encod

ALIGNMENTS

RESULT 1			
AD289039	standard;	DNA;	530 BP.
ID XX			
AC XX			
DT XX	28-JUL-2005	(first entry)	
DE XX			Pig growth factor II (GF II) gene, seq id 2.
KW XX			Growth; biochip; swine; hog raising; growth factor II; gene; ds.
XX			Sub scrofa; Kagoshima Berkshire.
XX			OS XX
PN XX			US2005112597-A1.
PD XX			26-MAY-2005.
PF XX			26-FEB-2004;
PR XX			24-NOV-2003; 2003KR-00083653.

(KIMC/)	KIM C.
PA	(YEOJ/)
PA	VEO J.
PA	(LEEJ/)
PA	LEE J.
PA	(SONGJ/)
PA	SONG Y.
PA	(CHOK/)
PA	CHO K.
PA	(CHUNJ/)
PA	CHUNG K.
PA	(KIMI/)
PA	KIM I.
PA	(JINJS/)
PA	JIN S.
PA	(JINP/)
PA	PARK S.
PA	(PARKM/)
PA	PARK M.
PA	(JUNGJ/)
PA	JUNG J.
PA	(LEEJM/)
PA	LEE M.
PA	(KWONJ/)
PA	KWON E.
PA	(CHOE/)
PA	CHO E.
PA	(CHOH/)
PA	CHO H.
PA	(SHINJ/)
PA	SHIN S.
PA	(NAMH/)
PA	NAM H.
PA	(HONGJ/)
PA	HONG Y.
PA	(HONGS/)
PA	HONG S.
PA	(KANGJ/)
PA	KANG Y.
PA	(HAYY/)
PA	HAY Y.

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OM nucleic - nucleic search, using bw model

Run on: February 20, 2006, 10:51:20 ; Search time 3140.18 Seconds
 (without alignments)

Title: US-10-785-981-2

Perfect score: 530

Sequence: 1 gctgactgtatcgggaaatc....tagggccattgtaaaatccctgg 530

Scoring table: IDENTITY_NUC Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

Database :	EST:*	gb_est1:*	gb_est2:*	gb_est3:*	gb_htc:*	gb_est4:*	gb_est5:*	gb_est6:*	gb_est7:*	gb_gb81:*	gb_gb81:*	gb_gb81:*
	1:	2:	3:	4:	5:	6:	7:	8:	9:	10:	11:	
	gb_est1:*	gb_est2:*	gb_est3:*	gb_htc:*	gb_est4:*	gb_est5:*	gb_est6:*	gb_est7:*	gb_gb81:*	gb_gb81:*	gb_gb81:*	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Source	FEATURES	Location/Qualifiers
-- 1	462.8	87.3	5667	DQ052205	Homo sapi			
2	462.8	87.3	5667	DQ052206	Pan trogl			
3	450	84.9	2674	AK041122	Mus muscu			
4	447.6	84.5	752	DN423235	DN42126-0			
5	431.2	81.4	3339	AK029328	Mus muscu			
6	429.2	81.0	623	DN423628	DN4216-0			
7	427.6	80.7	648	DN421412	DN421412			
8	427.6	80.7	771	DN455844	DN4216-0			
9	424.4	80.1	5820	DQ059772	Homo sapi			
10	422.4	79.7	650	DN424241	DN4216-1			
11	421.6	79.5	5814	DQ052207	Homo sapi			
12	418	78.9	5814	DQ052208	Pan trogl			
13	416.4	78.6	6062	HSMB02948	Homo sapi			
14	415.2	78.3	785	DN423007	DN4216-0			
c 15	412.4	77.8	675	CD621454	CD621454			
16	398.8	75.2	710	DN421704	DN421704			
17	374.8	70.7	817	CX901213	JGI CA09			
18	369	69.6	493	BUS87960	BUS87960			
19	368.2	69.5	5805	DQ029773	Pan trogl			
20	367.8	69.4	539	AW918573	AW918573			
21	367	69.2	649	DN421699	DN421699			
22	366.6	69.2	667	DN421346	DN421346			

ALIGNMENTS

RESULT 1	DQ052205	5667 bp DNA linear GSS 02-JUN-2005
LOCUS	Homo sapiens MYH1 gene, VIRTUAL TRANSCRIPT, partial sequence.	
DEFINITION	Genomic survey sequence.	
ACCESSION	DQ052205	
VERSION	DQ052205.1	
KEYWORDS	GI:66905676	
SOURCE	Homo sapiens (human)	
ORGANISM	Eukarya; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo	
REFERENCE	1 (bases 1 to 5667)	
AUTHORS	Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Pledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.	
TITLE	Direct Submission (05-NAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA	
JOURNAL	A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees (er) PLoS Biol. 3 (6), e170 (2005)	
PUBLISHED	15863325	
REFERENCE	2 (bases 1 to 5667)	
AUTHORS	Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Pledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.	
TITLE	Direct Submission (05-NAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA	
JOURNAL	This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.	
COMMENT		

Query Match 87.3% Score 462.8; DB 11; Length 5667;
 Best Local Similarity 92.9%; Pred. No. 1..3e-125;
 Matches 485; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

/locus_tag="HC20221"

ORIGIN

QY	9	ATCGGGAGAATCAGCTTAATCACCGGAGATCCGGGAAGAAAGACTGTGAAACA	68	gene	/db_xref="taxon: 9598"
Db	505	ATCGGGAGAATCAGCTTAATCACCGGAGATTCGGAGACTGTGAAACA	565	ORIGIN	<1...>567
QY	69	CGAACGGTGTICATCCAGTACTTGCCACATGCCGTCACTGGGAGAAGAAGGG	128	Query Match	87.3%
Db	566	CCAAAGCGTGTICATCCAGTACTTGCCACATGCCGTCACTGGGAGAAGAAGGG	625	Best Local Similarity	92.9%
QY	129	AACCTACTCTGGAAATAATCGGGGACTCTGGAAATCCAACTTGCAGTTGAGT	188	Matches	485;
Db	626	AAGTTACTCTGGAAATAATCGGGGACTCTGGAAATCACTCGTGCACCC	685	Conservative	0;
QY	189	TGCTCGAGGSCCTTGCAACGCCAGCTGGAAAGCAACTCCCTCGCTTGTGA	248	Missmatches	37;
Db	685	TACTGGAGGCTTGGCAAGCCAGCTGGAAAGCAACTCCCTCGCTTGTGA	745	Indels	0;
QY	249	AATTATCAGGATCCACTTGGTACCTGGGACTGGGAAGCTGGCTGACAACT	308	Gaps	0;
Db	746	AATTATCAGGATCCACTTGGTACCTGGGACTGGGAAGCTGGCTGACAACT	805		
QY	309	ATCPTCTAAGAAAGCTTAAGTCACTTCCAGTAAAGGAGAACTCCACATT	368		
Db	806	ATCPTCTGAGAAGCTTAAGTCACTTCCAGTAAAGGAGAACTCCACATT	865		
QY	369	TTATCAGATCATGCTTAACAGAACGCCAGCTTAAGTAACTCTCTGATCACC	428		
Db	866	TTATCAGATCATGCTTAACAGAACGCCAGCTTAAGTAACTCTCTGATCACC	925		
QY	429	ACCCATATGACTAGCCCTGTCTGTCAGTCAAGGGGAGATCAGTGTGATGAC	488		
Db	926	ACCCATACGTTATGCCCTGTCTGTCAGTCAAGGGGAGATCAGTGTGATGAC	985		
QY	489	AAGCAGGAGGTGATGCCACAGATAGTGCATTGAAATCTGG	530		
Db	986	AAGCAGGAGGTGATGCCACAGATAGTGCATTGAAATCTGG	1027		
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RESULT 2	DQ052206	DQ052206	5667 bp	DNA linear	GSS 02-JUN-2005
DEFINITION	Pan troglodytes MYH1 gene, VIRTUAL TRANSCRIPT, Partial sequence.				
ACCESSION	DQ052206				
VERSION	DQ052206.1				
KEYWORDS	GI:66905677				
SOURCE	Pan troglodytes (chimpanzee)				
ORGANISM	Zukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Burchontogires; Primates; Catarrhini; Hominidae; Pan				
REFERENCE	1 (bases 1 to 5667)				
AUTHORS	Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.				
TITLE	A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees (er) PLoS Biol. 3 (6), E170 (2005)				
JOURNAL	15869325				
PUBLMED	2 (bases 1 to 5667)				
AUTHORS	Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.				
TITLE	Direct Submission (05-MAY-2005) Celera Genomics, 45 West Glide Drive, Rockville, MD 20850, USA				
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.				
FEATURES	Location/Qualifiers				
source	1. 5667 /organism="Pan troglodytes"				
	/mol_type="genomic DNA"				

Result No.	Score	Query Match	Length	DB ID	Description
1	470.8	88.8	5925	3 US-09-949-016-5233	Sequence 5233, AP
2	424.4	80.1	6016	3 US-09-949-016-1054	Sequence 1054, AP
3	424.4	80.1	6016	3 US-09-949-016-2264	Sequence 2264, AP
4	362.4	68.4	6011	3 US-09-949-016-3017	Sequence 3017, AP
5	347.6	65.6	5992	3 US-09-949-016-346	Sequence 546, AP
6	347.6	65.6	5992	3 US-09-949-016-2263	Sequence 2263, AP
7	328.4	62.0	5661	3 US-09-938-105-2	Sequence 2, Appl
8	308.0	58.1	6008	3 US-09-949-016-5058	Sequence 5058, AP
9	144	27.2	6644	3 US-08-875-435B-5	Sequence 5, Appl
10	141.4	26.7	5919	3 US-08-875-435B-2	Sequence 2, Appl
11	141.2	26.6	6175	3 US-08-875-435B-1	Sequence 1, Appl
12	141	26.6	5883	3 US-09-949-016-5001	Sequence 5001, AP
13	139.2	26.3	5574	3 US-09-917-254-40	Sequence 40, Appl
14	139.2	26.3	6861	3 US-09-949-016-1240	Sequence 1240, AP
15	139.2	26.3	6861	3 US-09-949-016-1241	Sequence 1241, AP
16	139	26.3	6861	3 US-09-949-016-1242	Sequence 1242, AP
17	123.8	23.4	7596	3 US-09-023-655-1463	Sequence 1463, AP
18	122.2	23.1	7453	3 US-09-620-312D-248	Sequence 248, AP
19	109.4	20.6	3581	3 US-09-949-016-4965	Sequence 4965, AP
20	105.2	19.8	28355	3 US-09-949-016-16975	Sequence 16975, A
21	105	19.8	4668	3 US-09-949-016-4522	Sequence 4522, AP
22	98.2	18.5	7501	3 US-09-620-312D-249	Sequence 249, AP
23	94.6	17.8	30271	3 US-09-949-016-12796	Sequence 12796, A
24	94.6	17.8	30272	3 US-09-949-016-14006	Sequence 14006, A

RESULT 3
US-09-949-016-2264
Sequence 104, Application US/09949016
PATENT NO. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIORITY APPLICATION NUMBER: 60/1307
PRIOR FILING DATE: 2000-04-14
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ For Windows Version 4.0
SEQ ID NO 2264
LENGTH: 6016
TYPE: DNA
ORGANISM: Human
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1054
LENGTH: 6016
TYPE: DNA
ORGANISM: Human
NUMBER OF SEQ ID NOS: 207012

Query Match 80.1%; Score 424.4; DB 3; Length 6016;
Best Local Similarity 87.5%; Pred. No. 5.3e-125; Mismatches 0; Indels 0; Gaps 0;

Matches 464; Conservative 0; MisMatches 66; Indels 0; Gaps 0;

Db 969 CCACATATTTCATGAACTTCAACAGGGAAACTGGCTTCGTGAT 797
Qy 421 CACCAACCCATCTTCAAGAAGCTTAGAGTCACTTCCGCTAAAGGAAGCTA 360
Db 1029 CACCAACCCATCTTCCGCTAAAGGCTGAAAGCTA 857
Qy 481 TGATGACCAGAGGAGTGATGGCCACAGATACTGCCATTGAAATCCCTGG 530
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RESULT 3
US-09-949-016-2264
Sequence 2264, Application US/09949016
PATENT NO. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIORITY APPLICATION NUMBER: 60/1307
PRIOR FILING DATE: 2000-04-14
CURRENT APPLICATION NUMBER: 60/1307
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ For Windows Version 4.0
SEQ ID NO 2264
LENGTH: 6016
TYPE: DNA
ORGANISM: Human
NUMBER OF SEQ ID NOS: 207012

Query Match 80.1%; Score 424.4; DB 3; Length 6016;
Best Local Similarity 87.5%; Pred. No. 5.3e-125; Mismatches 66; Indels 0; Gaps 0;

Matches 464; Conservative 0; MisMatches 66; Indels 0; Gaps 0;

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Db 669 TGTGAAACCGAACGGTGTCACTCCAGATCTTCGCACTCGCGTCACTGGGAGAGAA 728

Qy 1 GCTGACTGTATGGGAAATCTAGITCTATTAATCACGGAGAACTCGGGCGAGAAAGC 60
Db 609 GCTGACTGTATGGGAAATCTAGITCTATTAATCACGGAGAACTCGGGCGAGAAAGC 668
Qy 61 TGTGAAACCGAACGGTGTCACTCCAGATCTTCGCACTCGCGTCACTGGGAGAGAA 120
Db 669 TGTGAAACCGAACGGTGTCACTCCAGATCTTCGCACTCGCGTCACTGGGAGAGAA 728

Db 789 TAACCCCTACTGCGAGCTTCGCAATCGAAAGTCAAGTCACTTCGCAATCGAAAGTCA 848
Qy 121 GAAAGGGAACTTACTCCGGCAAATATGGGGGAACTGGCAAGATCATCATCGTC 180
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Qy 361 CCACATTTTATCAAGTCACTTCGCAACGAGCTCATGAAATGCTCTGTGAT 420
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Qy 301 CGAAACATATCTCTAGAAAGTCACTTCGCAATCGAAAGGCAAAAGGCTA 360
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Qy 361 CCACATTTTATCAAGTCACTTCGCAACGAGCTCATGAAATGCTCTGTGAT 420
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24	162.8	30.7	6915	7	US-10-188-186-47	Sequence 47, APP1
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26	141	26.6	6354	5	US-10-084-817-100	Sequence 158, APP1
27	141	26.6	7274	9	US-10-696-909-A-8	Sequence 48, APP1
28	141	26.6	7396	6	US-10-028-248A-35	Sequence 35, APP1
29	141	26.6	7396	7	US-10-107-882-55	Sequence 35, APP1
30	141	26.6	2486	8	US-10-357-930-22131	Sequence 22131, A
31	139.2	26.3	2486	8	US-10-357-930-227993	Sequence 27993, A
32	139.2	26.3	2535	3	US-09-927-597-13	Sequence 13, APP1
33	139.2	26.3	2535	9	US-10-486-057-13	Sequence 13, APP1
34	139.2	26.3	6655	7	US-10-296-115-526	Sequence 526, APP1
35	139.2	26.3	6861	5	US-10-171-11-161	Sequence 161, APP1
36	139.2	26.3	6861	6	US-10-341-434-102	Sequence 102, APP1
37	139.2	26.3	6861	9	US-10-923-035-18	Sequence 18, APP1
38	139.2	26.3	6900	5	US-10-171-11-163	Sequence 163, APP1
39	139.2	26.3	6900	7	US-10-764-425-13	Sequence 13, APP1
40	139.2	26.3	11065	5	US-10-116-802-14	Sequence 14, APP1
41	139.2	26.3	2097	3	US-09-927-597-5	Sequence 5, APP1
42	136.6	25.8	2097	3	US-10-486-057-5	Sequence 5, APP1
43	136.6	25.8	2316	9	US-09-927-597-7	Sequence 7, APP1
44	136.6	25.8	2316	9	US-10-486-057-7	Sequence 7, APP1
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ALIGNMENTS

RESULT 1
US-10-785-981-2

; Sequence 2, Application US/10785981
; Publication No. US20050112597A1

; GENERAL INFORMATION:
; APPLICANT: GYEONGSANNAM-DO
; CHULWOOK, KIM
; TITLE OF INVENTION: SCREENING EXPRESSION PROFILE OF GROWTH SPECIFIC GENES IN AND FUNCTIONAL CDNA CHIP PREPARED BY USING THE SAME
; FILE REFERENCE: 3884-0120P

; CURRENT APPLICATION NUMBER: US/10/785,981
; CURRENT FILING DATE: 2004-06-26
; PRIOR APPLICATION NUMBER: KR 2003-83653
; PRIOR FILING DATE: 2003-11-24

; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2

; SEQ ID NO: 2

; LENGTH: 530

; TYPE: DNA

; ORGANISM: Kagoshima Berkshire

; US-10-785-981-2

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	530	100.0	530	9	US-10-785-981-2
2	530	100.0	530	9	US-10-789-723-2
3	530	100.0	530	9	US-10-786-052-2
4	470.8	88.8	5925	9	US-10-335-053-26
5	433.4	81.6	5874	9	US-10-450-763-21224
6	421.6	79.5	6010	8	US-10-723-860-57
7	421.6	79.5	6010	8	US-10-723-860-105
8	421.6	79.5	6010	8	US-10-723-860-1827
9	421.6	79.5	6010	8	US-10-723-860-4858
10	416.4	78.6	5956	9	US-10-783-721-100
11	362.4	68.4	6523	6	US-10-062-674-1980
12	320.4	60.5	5886	8	US-10-798-037-3
13	322.4	60.5	12801	8	US-10-798-037-5
14	313.2	59.1	5918	5	US-10-198-846-13875
15	308	58.1	4775	7	US-10-336-472-17
16	308	58.1	5780	7	US-10-336-472-19
17	308	58.1	6008	7	US-10-336-472-21
18	308	58.1	6008	7	US-10-717-597-197
19	301.6	56.9	5925	7	US-10-191-803-104
20	248.8	46.9	6149	7	US-10-188-186-95
21	244.2	46.1	716	6	US-10-257-86A-65
22	227.2	42.9	6237	9	US-10-450-763-12161
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					241 CTTTGTAAATTCACTAGGATCCACTGGTACCACTGGAAAGCTGGCTGACAT
					241 CTTTGTAAATTCACTAGGATCCACTGGTACCACTGGAAAGCTGGCTGACAT

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OM nucleic - nucleic search, using bw model

Run on: February 20, 2006, 11:27:30 ; Search time 404.955 seconds
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Perfect score: 530

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Scoring table: IDENTITY_NUC
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Total number of hits satisfying chosen parameters: 14408646

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13: /cgn2_6/ptodata/2/pubna/US60_NEW_PUB.seq;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	470.0	88.8	5925	12 US-11-000-688-1358	Sequence 1358, Ap
2	416.4	78.6	6062	12 US-11-050-888-13	Sequence 13, App1
3	352.8	66.6	6035	12 US-11-336-527-3751	Sequence 3751, Ap
4	320.4	62.0	6021	12 US-11-336-527-274	Sequence 274, App
5	303.6	57.3	5941	12 US-11-336-527-275	Sequence 275, App
6	146.6	27.5	6056	12 US-11-336-527-2285	Sequence 2285, App
7	145.6	27.5	6377	12 US-11-059-834-57	Sequence 57, App1
8	144.2	27.4	7355	12 US-11-059-834-47	Sequence 47, App1
9	144.8	27.3	6442	8 US-11-059-834-55	Sequence 55, App1
10	144.2	27.2	6786	12 US-11-059-834-59	Sequence 59, App1
11	141.2	26.6	7474	12 US-11-059-834-49	Sequence 49, App1
12	139.2	26.3	6300	12 US-11-000-688-1142	Sequence 1142, Ap
13	138.8	26.2	4239	8 US-10-995-561-148	Sequence 148, App
14	138.8	26.2	6025	8 US-10-995-561-143	Sequence 143, App
15	138.8	26.2	6148	8 US-10-995-561-147	Sequence 147, App
16	138.8	26.2	6187	8 US-10-995-561-144	Sequence 144, App
17	138.8	26.2	6886	8 US-10-995-561-149	Sequence 149, App
18	138.8	26.2	6925	8 US-10-995-561-145	Sequence 145, App
19	138	26.0	6185	8 US-10-995-561-146	Sequence 146, App
20	135	25.5	2097	12 US-11-136-527-3099	Sequence 3099, Ap

ALIGNMENTS

RESULT 1
US-11-000-688-1358
; Sequence 1358, Application US/11000688
; Publication No. US20050287541A1
; GENERAL INFORMATION:
; APPLICANT: BERTUCCI, Francois
; APPLICANT: HOULGAUTE, Remi
; APPLICANT: BIRNBAUM, Daniel
; TITUL OF INVENTION: GENE EXPRESSION PROFILING OF COLON CANCER WITH DNA ARRAYS
; FILE REFERENCE: 1423-R-03
; CURRENT APPLICATION NUMBER: US/11/000, 688
; CURRENT FILING DATE: 2004-12-01
; PRIOR APPLICATION NUMBER: US 60/525, 987
; PRIORITY FILING DATE: 2003-12-01
; NUMBER OF SEQ ID: NOS: 1596
; SEQ ID NO: 1358
; LENGTH: 5925
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial sequences: primer
; NAME/KEY: misc_feature
; LOCATION: (1)-(5925)
; OTHER INFORMATION: myosin, heavy polypeptide 1, skeletal muscle, adult (MYH1) gene.
US-11-000-688-1358

Query Match 88.8%; Score 470.8%; DB 12; Length 5925;
Best Local Similarity 93.0%; Pred. No. 7.2e-17;
Matches 493; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

1 GTGTGATCTGGAAAGTCACTTCATTCCGGAGATCCGGGCAACTCGCGCTACTGGGAGAAAGAC 60
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3 61 TGTGAACAGAACGAGCTGTCATCCAGTACTTCGCCAACATCGCGCTACTGGGAGAAAGAC 120
4 558 TGTGAACAGAACGAGCTGTCATCCAGTACTTCGCCAACATCGCGCTACTGGGAGAAAGAC 617
5 121 GAGGGAGAACCTACTCTGGAAAAATGCGGGATCTGGAGATCATCATCATGTC 180

618 GAGGAGAAGGTACTTGGCAAATGGGAACTTGGAAGATCATCGTGC 677
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 858 TCATATTTATCAGATCTAGATCTAGACTTCCAGTAACTGGAACTGGTCTGTGAT 917

RESULT 3
 US-11-136-527-3751
 Sequence 3751, Application US/11136527
 Publication No. US/0050287570A1
 GENERAL INFORMATION:
 APPLICANT: Wyeth
 MOUNTS, William M
 ATTORNEY: Mounts, William M
 TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
 FILE REFERENCE: 031896_0410000 (AM101086)
 CURRENT APPLICATION NUMBER: US/11/136,527
 CURRENT FILING DATE: 2005-05-25
 PRIORITY APPLICATION NUMBER: US 60/574,294
 PRIORITY FILING DATE: 2005-05-26
 NUMBER OF SEQ ID NOS: 362830
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 3751
 LENGTH: 6035
 TYPE: DNA
 ORGANISM: Rattus norvegicus
 US-11-136-527-3751

Query Match Score 416.4; DB 12; Length 6062;
 Best Local Similarity 86.6%; Pred. No. 5.1e-111; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTGACTGATGGGAAATAGTCATCTGAAATCGCCAAATGGGAAAGAC 60
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 Db 882 TGAACATATCTCTGGAAAAGTCAGACTCACCTCCAGTCACTTCCAGTAAATGGGAAAGAC 941
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BD017804 Novel gen	6	BD017804
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AL591593 Zebrafish	5	AL591593
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BD079915 ACCESSION		
BD079915.1 GI:22625518 VERBISON		
JP 2001156009-A/581. KEYWORDS		
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butelostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.		
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Old, L.J., Scanlan, M.J., Stockert, E., Gure, A., Chen, Y.T., Gout, I., Oghare, M., Obata, Y., Pfreundschuh, M., Tureci, O. and Sahin, U.		
TITLE		
JOURNAL		
LUDWIG INSTITUTE FOR CANCER RESEARCH COMMENT OS Homo sapiens (human)		
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COMMENT PN JP 2001156009-A/581		
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PD 25-SEP-2001		
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PP 17-JUL-1997		
PR 17-JUL-1997		
PR 10-OCT-1997		
PR 11-OCT-1997		
PR 60/061765, 10-OCT-1997 US 08/948705 PR		
J OLD, MATTHEW J SCANLAN, ELISABETH STOCKERT, ALI GURE, YAO PI CHEN, PI IVAN GOUT, MICHAEL O'HARE, YUICHI OBATA, MICHAEL PFREUNDSCHUH, PI OZLEM TURECI, PI UGUR SAHIN PC		
G01N3/574, A61K38/00, A61K39/395, A61K45/00, A61K48/00, PC A61B5/00, PC C07K14/82, C07K16/32, C12N15/09/C07K16/46, C12P21/08, A61K37/02, PC C12N15/00 CC Cancer-associated nucleic acids and polypeptides. FH Key Location/Qualifiers		
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1. .1427		

Page 2

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Db	164 TCAATGTCACCTACAAGAGAGATCTCA
Qy	121 GAACTTAATTCGAGTTTCAATGATGCTCTGA
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Qy	181 TTACCTAGGGTAAACCTGACAGCRAAATGA
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Qy	241 AATGTTGCAATCTGTGTTTCTGGGGCATTTGA
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Qy	301 CGTCATAATTCTTTAGTAGCRAAATGATGATCT
Db	404 CGTCATAATTCTTTAGTAGCRAAATGATGATCT
Qy	361 AAAGCCATGGCAACTACCTTAACTACAGAAAGG
Db	464 AGAACCTGGCAACTACCTTAACTACAGAAAGG
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Qy	-TCAGTGTACAGATGAAATCTCAGAAAGGGGG
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Qy	540 TGATGACCAA 549
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LOCUS	1677 bp
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ACCESSION	7839
VERSION	CQ721905
KEYWORDS	CQ721905.1 GI:42282762
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Crani- Mammalia; Eutheria; Euarchontogli- Hominidae; Homo.
REFERENCE	1
AUTHORS	Venter,C.J., Adams,M.C., Li,P.W. a-
TITLE	titles, such as nucleic acid arrays, thereof
JOURNAL	Patent: WO 02068579-A 7839 06-SEP- PE Corporation (NY) (US)
FEATURES	Location /Qualifiers Source
	1. 1677 /organism="Homo sapiens" /mol type="unassigned signed DNA" /orgnism="Homo sapiens"

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OM nucleic - nucleic search, using sw model

Run on: February 20, 2006, 10:51:20 ; Search time 3489,74 Seconds
 (without alignments)

Title: US-10-785-981-3

Perfect score: 589

Sequence: 1 gttgttcctttaatcatgt.....tagtccattgaaatccctgg 589

Scoring table: IDENTITY_NUC Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0\$ Maximum Match 100\$ Listing first 45 summaries

Result No.	Score	Query	Match	Length	DB	ID	Description
1	528.4	EST:*	gb_est1:*	755	2	BG031674	
2	528.4	EST:*	gb_est2:*	755	2	BG031674	
3	528.4	EST:*	gb_est3:*	755	2	BG031674	
4	528.4	HTC:*	gb_htc:*	755	2	BG031674	
5	528.4	EST:*	gb_est4:*	755	2	BG031674	
6	528.4	EST:*	gb_est5:*	755	2	BG031674	
7	528.4	EST:*	gb_est6:*	755	2	BG031674	
8	528.4	EST:*	gb_est7:*	755	2	BG031674	
9	528.4	GB_GSS1:*	gb_gss1:*	755	2	BG031674	
10	528.4	GB_GSS3:*	gb_gss3:*	755	2	BG031674	
11	527.6			1012	1	AL560753	
8	527.4			1112	3	BM802677	
9	526.8			615	2	BE175655	
10	526.8			908	2	BG779206	
11	526.8			1035	1	AL528352	
12	525.2			1932	11	DQ053605	
13	525			862	2	BG166586	
14	524			89.0	1	AL529078	
15	517.6			87.9	702	BG678319	
16	479			81.4	1	AL548432	
17	478.4			81.2	2	BP132189	
18	478			88.4	2	BF984746	
19	428.4			74.8	485	BW766987	
20	428.4			72.7	1	AW386704	
21	419			604	1	AW581575	
c	22			423	9	AQ206754	

CE134508 UI-HF-CBO
 BE175777 RC5-RT058
 278223 HS278323 Hu
 DN50090 12627294 M
 AQ207000 HS342 A
 BG403231 602418679
 CO581479 ILLUMIGEN
 BM930680 UI-H-DIO-
 BE636484 PM4-CT039
 BE773649 QV1-FT016
 BB773939 QV1-FT016
 COB94304 BoyGen 22
 BP213807 601847859
 AW95225 EST34495
 DN872098 nad17911.
 BG164923 602343548
 BE887500 501508149
 BB816524 QVO-FN006
 AQ241682 RPC111-12
 AJ662831 AJ662831
 CR835329 4059712 B
 AQ717690 HS5496 B
 BE336026 601062461

ALIGNMENTS

RESULT 1

LOCUS	DEFINITION	mRNA sequence.
BG031674	602300827F1 NIH_MGC_87	Homo sapiens cDNA clone IMAGE:4402182 5' ,
BG031674		mRNA sequence.
ACCESSION	BG031674	
VERSION	EST.	GI:12422197
KEYWORDS	Homo sapiens (human)	
SOURCE	Homo sapiens	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.	
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-z@mail.nih.gov Tissue Procurement: DCTD/DRP cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LILNL at: http://image.llnl.gov Place: LILNL1010 row: f column: 07 High quality sequence stop: 717. Location/Qualifiers	1. 755
REFERENCE	1 (bases 1 to 755)	
AUTHORS	NIH-MGC	http://mgc.nci.nih.gov/
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)	
JOURNAL	Unpublished (1999)	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	528.4	EST:*	gb_est1:*	755	2	BG031674	
2	528.4	EST:*	gb_est2:*	755	2	BG031674	
3	528.4	EST:*	gb_est3:*	755	2	BG031674	
4	528.4	HTC:*	gb_htc:*	755	2	BG031674	
5	528.4	EST:*	gb_est4:*	755	2	BG031674	
6	528.4	EST:*	gb_est5:*	755	2	BG031674	
7	528.4	EST:*	gb_est6:*	755	2	BG031674	
8	528.4	EST:*	gb_est7:*	755	2	BG031674	
9	528.4	GB_GSS1:*	gb_gss1:*	755	2	BG031674	
10	528.4	GB_GSS3:*	gb_gss3:*	755	2	BG031674	
11	527.6			1012	1	AL560753	
8	527.4			1112	3	BM802677	
9	526.8			615	2	BE175655	
10	526.8			908	2	BG779206	
11	526.8			1035	1	AL528352	
12	525.2			1932	11	DQ053605	
13	525			862	2	BG166586	
14	524			89.0	1	AL529078	
15	517.6			87.9	702	BG678319	
16	479			81.4	1	AL548432	
17	478.4			81.2	2	BP132189	
18	478			88.4	2	BF984746	
19	428.4			74.8	485	BW766987	
20	428.4			72.7	1	AW386704	
21	419			604	1	AW581575	
c	22			423	9	AQ206754	

Query Match Score 528.4; DB 2; Length 755;

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OM nucleic - nucleic search, using sw mode.

Run on: February 20, 2006, 10:32:49 ; Search time 499.848 Seconds
 7853.391 Million cell updates/sec

Title: US-10-785-981-3

Pefect score: 589

Sequence: 1 gttgttcctttaatatgtat.....taggccattgaatccctgg 589

Scoring table: IDENTITY NUC Gapop 10.-0 , Gapext 1.0

Searched: 4996997 seqs, 3312346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :	N Geneseq 21:*
	1: geneseqn1980s:*
	2: geneseqn1990s:*
	3: geneseqn2000s:*
	4: geneseqn2001as:*
	5: geneseqn2001bs:*
	6: geneseqn2002as:*
	7: geneseqn2002bs:*
	8: geneseqn2003as:*
	9: geneseqn2003bs:*
	10: geneseqn2004cs:*
	11: geneseqn2004ds:*
	12: geneseqn2004as:*
	13: geneseqn2004bs:*
	14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	589	100.0	589	14	ADZ89040	Adz89040 Pig growt
2	589	100.0	589	14	ADZ79333	Adz79333 Swine gro
3	589	100.0	589	14	ADZ7170	Adz7170 Pig growt
4	528.4	89.7	1427	2	AAK40181	Aak40181 Lung canc
5	528.4	89.7	1932	13	ADQ89911	Adq89911 Antagonis
6	528.4	89.7	2357	4	AAF60005	Aaf60005 Human syn
7	528.4	89.7	2414	6	ABL89966	Abi89966 Human pol
8	528.4	89.7	2703	4	AAI58275	Aai58275 Human pol
9	528.4	89.7	2703	5	ADQ98482	Adq98482 DNA encod
10	528.4	89.7	2703	9	ADB48242	Adb48242 Novel hum
11	528.4	89.7	6499	4	AAK86748	Aak86748 Human imm
12	526.8	89.4	2451	10	ADI40392	Adi40392 Human pur
13	517.4	87.8	2410	4	AAI60061	Aai60061 Human pol
14	474.8	80.6	610	14	ACI57351	aci57351 Human col
15	391.6	66.5	2734	5	AAS84622	Aas84622 DNA encod
16	353.8	60.1	776	4	AAI97610	Aai97610 Human neu
17	137	23.3	396	4	AAF9459	Aaf9459 Human ova
18	137	23.3	396	6	ABL48909	Abi48909 Ovarian C
19	137	23.3	396	6	ABT03226	Abt03226 Human ova

ALIGNMENTS

RESULT 1	XX	XX	XX	XX	XX	XX
ID ADZ89040	standard; DNA;	589 BP.	AC ADZ89040;	DT DT	28-JUL-2005	(first entry)
AB18996 Drosophil						
Abi19004 Drosophil						
Ach21529 Human adu						
Aas84621 DNA encod						
Adz89041 Pig growt						
Adz79334 Swine gro						
Adz71717 Pig growt						
Adw95930 cDNA enco						
Adx15796 DNA encod						
Aox25983 Novel cel						
Adq22038 Human sof						
Adq22007 Human sof						

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	589	100.0	589	14	ADZ89040	Adz89040 Pig growt
2	589	100.0	589	14	ADZ79333	Adz79333 Swine gro
3	589	100.0	589	14	ADZ7170	Adz7170 Pig growt
4	528.4	89.7	1427	2	AAK40181	Aak40181 Lung canc
5	528.4	89.7	1932	13	ADQ89911	Adq89911 Antagonis
6	528.4	89.7	2357	4	AAF60005	Aaf60005 Human syn
7	528.4	89.7	2414	6	ABL89966	Abi89966 Human pol
8	528.4	89.7	2703	4	AAI58275	Aai58275 Human pol
9	528.4	89.7	2703	5	ADQ98482	Adq98482 DNA encod
10	528.4	89.7	2703	9	ADB48242	Adb48242 Novel hum
11	528.4	89.7	6499	4	AAK86748	Aak86748 Human imm
12	526.8	89.4	2451	10	ADI40392	Adi40392 Human pur
13	517.4	87.8	2410	4	AAI60061	Aai60061 Human pol
14	474.8	80.6	610	14	ACI57351	aci57351 Human col
15	391.6	66.5	2734	5	AAS84622	Aas84622 DNA encod
16	353.8	60.1	776	4	AAI97610	Aai97610 Human neu
17	137	23.3	396	4	AAF9459	Aaf9459 Human ova
18	137	23.3	396	6	ABL48909	Abi48909 Ovarian C
19	137	23.3	396	6	ABT03226	Abt03226 Human ova

PN US2005112597-A1.

XX XX XX XX XX XX

PD 26-MAY-2005.

PF 26-FEB-2004; 2004US-00785981.

XX XX XX XX XX XX

PR 24-NOV-2003; 2003KR-00083633.

XX XX XX XX XX XX

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	589	100.0	589	14	ADZ89040	Adz89040 Pig growt
2	589	100.0	589	14	ADZ79333	Adz79333 Swine gro
3	589	100.0	589	14	ADZ7170	Adz7170 Pig growt
4	528.4	89.7	1427	2	AAK40181	Aak40181 Lung canc
5	528.4	89.7	1932	13	ADQ89911	Adq89911 Antagonis
6	528.4	89.7	2357	4	AAF60005	Aaf60005 Human syn
7	528.4	89.7	2414	6	ABL89966	Abi89966 Human pol
8	528.4	89.7	2703	4	AAI58275	Aai58275 Human pol
9	528.4	89.7	2703	5	ADQ98482	Adq98482 DNA encod
10	528.4	89.7	2703	9	ADB48242	Adb48242 Novel hum
11	528.4	89.7	6499	4	AAK86748	Aak86748 Human imm
12	526.8	89.4	2451	10	ADI40392	Adi40392 Human pur
13	517.4	87.8	2410	4	AAI60061	Aai60061 Human pol
14	474.8	80.6	610	14	ACI57351	aci57351 Human col
15	391.6	66.5	2734	5	AAS84622	Aas84622 DNA encod
16	353.8	60.1	776	4	AAI97610	Aai97610 Human neu
17	137	23.3	396	4	AAF9459	Aaf9459 Human ova
18	137	23.3	396	6	ABL48909	Abi48909 Ovarian C
19	137	23.3	396	6	ABT03226	Abt03226 Human ova

PA (KIMC/) KIM C.

PA (YEONJ/) YEO J.

PA (LEEJ/) LEE J.

PA (SONG/) SONG Y.

PA (CHOK/) CHO K.

PA (CHUNGK/) CHUNG K.

PA (KIMI/) KIM I.

PA (JINS/) JIN S.

PA (PARK/) PARK S.

PA (JUNG/) JUNG J.

PA (LEEJ/) LEE M.

PA (KMON/) KWON B.

PA (CHOE/) HO E.

PA (CHOH/) CHO H.

PA (SHINN/) SHIN S.

PA (NAMH/) NAM H.

PA (HONGJ/) HONG Y.

PA (HONGS/) HONG S.

PA (KANGJ/) KANG Y.

PA (HAYY/) HA Y.

PA	(ROUJ/)	ROU J.	QY	541	GATGACCAAGAGGGCTGTGGCCACAGATAGTGCATTGAAATCCTGG	589
PA	(KWA/C/)	KWACK S.	Db	541	GATGACCAAGAGGGCTGTGGCCACAGATAGTGCATTGAAATCCTGG	589
PA	(CHOI/)	CHOI I.				
PA	(KIMB/)	KIM B.				
XX						
PI	Kim C,	Yeo J, Lee J, Song Y, Cho K, Chung K, Kim I, Jin S;	RESULT 2			
PI	Park S,	Jung J, Lee M, Kwon B, Cho E, Shin S, Nam H;	ADZ79333			
PI	Hong Y,	Kang Y, Ha Y, Rou J, Kwack S, Choi I, Kim B;	Swine growth factor GF-III cDNA for cDNA chip diagnostic method.			
XX	DR	ADZ79333 standard; cDNA; 589 BP.	XX			
XX	WPI: 2005-403340/41.		XX			
XX	Functional cDNA chip useful for screening and function analysis of growth specific genes according to breeds and tissues of swine, comprises substrate and probe comprising growth specific genes in muscle and fat tissues of swine.	AC	ADZ79333;			
XX	Claim 2; SEQ ID NO 3; 8pp; English.	DT	28-JUL-2005 (first entry)			
XX	The invention relates to a functional cDNA chip (I) for screening and function analysis of growth specific genes according to breeds and tissues of swine, comprises a probe comprising growth specific genes in muscle and fat tissues of swine, and a substrate on which the probe is immobilized. Further disclosed is a kit (K1) useful for screening and functional analysis of growth specific gene according to breeds and tissues of swine, comprising (I) integrated in it, Cy5-dCTP or Cy3-dCTP bound cDNA from RNA of the tissue to be screened, a fluorescence scanning system, and a computer analysis system (II) and (K1) are useful for screening and function analysis of growth specific gene according to breeds and tissues of swine. (I) is useful in the swine improvement and breeding of a new breed, and in the hog raising industry. The current sequence represents the pig growth factor III (GF III) gene.	DE	Swine growth factor GF-III cDNA for cDNA chip diagnostic method.			
XX	Sequence 589 BP; 187 A; 110 C; 129 G; 163 T; 0 U; 0 Other;	XX	XX			
XX	Query Match 100.0%; Score 589; DB 14; Length 589;	XX	XX			
Best Local Similarity 100.0%; Pred. No. 4 9e-151;	Matches 589; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	XX	XX			
QY	1 GTTGTTCCCTTAAATATGATGTTGCCACAGCTGCATTCAGTCAGTCATGAAATATT	60	XX			
Db	1 GTTGTTCCCTTAAATATGATGTTGCCACAGCTGCATTCAGTCATGAAATATT	60	XX			
QY	61 TCCAATGTCGACCTTAACAGAGATACTCAAGCTCTTACTGTATCACATGAG	120	XX			
Db	61 TCCAATGTCGACCTTAACAGAGATACTCAAGCTCTTACTGTATCACATGAG	120	XX			
QY	121 GAAGTAATCTGCACTTCAATTGATCTCTGAATCTGATGAGCTCGATGTT	180	XX			
Db	121 GAAGTAATCTGCACTTCAATTGATCTCTGAATCTGATGAGCTCGATGTT	180	XX			
QY	181 TTACCTTAGGATGAAAACCTGACAGCAAATGAAAGTTTGTAAACCTGATGAAAGCA	240	XX			
Db	181 TTACCTAGGATGAAAACCTGACAGCAAATGAAAGTTTGTAAACCTGATGAAAGCA	240	XX			
QY	241 AATGTTGCAATCCGTGTTCTGGGGCATGATTCATGATTCATGCAACCCCTGCTGAC	300	XX			
Db	241 AATGTTGCAATCCGTGTTCTGGGGCATGATTCATGATTCATGCAACCCCTGCTGAC	300	XX			
QY	301 CGTCATATCCTTATGATGACCAATTGATCTCTTAATCTAGTTCTAGTCAGAAGA	360	XX			
Db	301 CGTCATATCCTTATGATGACCAATTGATCTCTTAATCTAGTTCTAGTCAGAAGA	360	XX			
QY	361 AAGACCATGCCAACTPACCTTTAACAGAGAGGGATAAACAGAAAAATAATGTAAATA	420	XX			
Db	361 AAGACCATGCCAACTPACCTTTAACAGAGAGGGATAAACAGAAAAATAATGTAAATA	420	XX			
QY	421 CCTTCAGAAAGAATTCTCAATTCTAAAGATGTTGCTGCTGCTGAGCTCTAAACAT	480	XX			
Db	421 CCTTCAGAAAGAATTCTCAATTCTAAAGATGTTGCTGCTGCTGAGCTCTAAACAT	480	XX			
QY	481 TCAGTGTACAGATGAAATCACAGGAGGGGACTAANGGAACACTACAGCTGTTAGCT	540	XX			
Db	481 TCAGTGTACAGATGAAATCACAGGAGGGGACTAANGGAACACTACAGCTGTTAGCT	540	XX			

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OM nucleic - nucleic search, using sw model

Run on: February 20, 2006, 11:15:29 ; Search time 144.524 Seconds
(without alignments)

7244.353 Million cell updates/sec

Title: US-10-785-981-3

Perfect score: 589

Sequence: 1 gttgttccttaatcatgat.....tagggccattgaaatccctgg 589

Scoring table: IDENTITY_NUC Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Result No.	Score	Query	Match	Length	DB	ID	Description
1	528.4	89.7	2703	3	US-09-620-312D-152		Sequence 152, App
2	137	23.3	396	3	US-09-640-173-150		Sequence 150, App
3	137	23.3	396	3	US-09-713-550-150		Sequence 150, App
4	137	23.3	396	3	US-09-825-294-150		Sequence 150, App
5	137	23.3	396	3	US-09-970-966-150		Sequence 150, App
6	48.2	8.2	886	3	US-09-270-767-151527		Sequence 15197, A
7	48.2	8.2	1514	3	US-09-270-767-15199		Sequence 15199, A
8	48	8.1	1141	3	US-09-806-708B-22		Sequence 28, App
9	43.6	7.4	5925	3	US-09-949-016-5233		Sequence 1523, App
10	40.4	6.9	6016	3	US-09-949-016-1054		Sequence 1054, App
11	40.4	6.9	6016	3	US-09-949-016-2264		Sequence 2264, App
12	39.4	6.7	1428	3	US-09-248-796A-1936		Sequence 1936, App
C 13	39.4	6.7	2082	3	US-09-248-796A-2564		Sequence 2564, App
14	38.8	6.6	601	3	US-09-949-016-40750		Sequence 40750, A
15	38.8	6.6	462589	3	US-09-949-016-12900		Sequence 12900, A
C 16	38.8	6.6	476044	3	US-09-949-016-12412		Sequence 12412, A
17	38.6	6.6	723	3	US-09-134-000C-2397		Sequence 2397, App
C 18	38.4	6.5	9048	3	US-09-973-273-4		Sequence 4, App
19	38.2	6.5	1368	3	US-09-248-796A-11323		Sequence 11323, A
20	38.2	6.5	1716	3	US-08-656-034-9		Sequence 9, App
21	38	6.5	1698	3	US-09-248-796A-1623		Sequence 1623, App
C 22	37.8	6.4	822	3	US-09-710-279-607		Sequence 607, App
C 23	37.8	6.4	2950	3	US-09-710-279-3349		Sequence 3349, App
C 24	37.8	6.4	3760	3	US-09-710-279-4029		Sequence 4029, App

ALIGNMENTS

RESULT 1
US-09-620-312D-152

; Sequence 155, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yuning
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radivoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; POLypeptides
; FILE REFERENCE: 78CIP2B
; CURRENT FILING NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOs: 1105
; SEQ ID NO 152
; LENGTH: 2703
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: CDS
; NAME/KEY: CDS
; LOCATION: (398) ..(2329)
US-09-620-312D-152

Query Match 89.7%; Score 528.4; DB 3; Length 2703;
Best Local Similarity 98.7%; Pred. No. 2, 3e-146;
Matches 543; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 1 GRTGTCCCTTAAATATGATGTTGCACAGCTGATGGAGACTATTGCACTATAATT 60

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	528.4	89.7	2703	3	US-09-620-312D-152		Sequence 152, App
2	137	23.3	396	3	US-09-640-173-150		Sequence 150, App
3	137	23.3	396	3	US-09-713-550-150		Sequence 150, App
4	137	23.3	396	3	US-09-825-294-150		Sequence 150, App
5	137	23.3	396	3	US-09-970-966-150		Sequence 150, App
6	48.2	8.2	886	3	US-09-270-767-151527		Sequence 15197, A
7	48.2	8.2	1514	3	US-09-270-767-15199		Sequence 15199, A
8	48	8.1	1141	3	US-09-806-708B-22		Sequence 28, App
9	43.6	7.4	5925	3	US-09-949-016-5233		Sequence 1523, App
10	40.4	6.9	6016	3	US-09-949-016-1054		Sequence 1054, App
11	40.4	6.9	6016	3	US-09-949-016-2264		Sequence 2264, App
12	39.4	6.7	1428	3	US-09-248-796A-1936		Sequence 1936, App
C 13	39.4	6.7	2082	3	US-09-248-796A-2564		Sequence 2564, App
14	38.8	6.6	601	3	US-09-949-016-40750		Sequence 40750, A
C 15	38.8	6.6	462589	3	US-09-949-016-12900		Sequence 12900, A
C 16	38.8	6.6	476044	3	US-09-949-016-12412		Sequence 12412, A
17	38.6	6.6	723	3	US-09-134-000C-2397		Sequence 2397, App
C 18	38.4	6.5	9048	3	US-09-973-273-4		Sequence 4, App
19	38.2	6.5	1368	3	US-09-248-796A-11323		Sequence 11323, A
20	38.2	6.5	1716	3	US-08-656-034-9		Sequence 9, App
21	38	6.5	1698	3	US-09-248-796A-1623		Sequence 1623, App
C 22	37.8	6.4	822	3	US-09-710-279-607		Sequence 607, App
C 23	37.8	6.4	2950	3	US-09-710-279-3349		Sequence 3349, App
C 24	37.8	6.4	3760	3	US-09-710-279-4029		Sequence 4029, App

Db 1118 GTTGTCCCTTAATATGGTGCACAGACTCAAGCTTACTGATCACATGAG 1177 Db 380 GAACTAATTCAGCAGTT 396

Qy 61 TCCATGTGCCACCTAACAGAGATACTCAAGCTTACTGATCACATGAG 120

Db 1178 TCCATGTGCCACCTAACAGAGATACTCAAGCTTACTGATCACATGAG 1237

Qy 121 GAACTAATTCAGCACTTCAATTGATGCTCGTAGCTGAGTCAGTCAAGAACG 180

Db 1238 GAACTAATTCAGCACTTCAATTGATGCTCGTAGCTGAGTCAGTCAAGAACG 1297

Qy 181 TTACCTAGGATGAAAACCTGACGCAAATGAACTTGGATAGTGAAAGCA 240

Db 1298 TTACCTAGGATGAAAACCTGACGCAAATGAAAGCTGATGAAAGCA 1357

Qy 241 AATGTGCATCCCTGTTGGGGCATGATCCATGGTATTGCAACCCPTGCTGAC 300

Db 1358 AATGTGCATCCCTGTTGGGGCATGATCCATGGTATTGCAACCCPTGCTGAC 1417

Qy 301 CGTCATATTCCTTAAAGATGAAACCAATTGATCTCTTAATGCTGAAAGA 360

Db 1418 CGTCATATTCCTTAAAGATGAAACCAATTGATCTCTTAATGCTGAAAGA 1477

Qy 361 AAGACCATGCCAACTACCTTAAACGAGAGGGATAAACAGAAAAATAATGTGAATA 420

Db 1478 AAGACCATGCCAACTACCTTAAACGAGAGGGATAAACAGAAAAATAATGTGAATA 1537

Qy 421 CCTTCAGAAAGAAATTCTAAAGAGCTTGGCTGCTGCTGAGCTCTAAACAT 480

Db 1538 CCTTCAGAAAGAAATTCTAAAGAGCTTGGCTGCTGCTGAGCTCTAAACAT 1597

Qy 481 -TCACTGTAACAGATGCAATCACCGAAAGGGGACTAACAGGAACTAACAGCTGTAAC 539

Db 1598 GTCACTGTAACAGATGCAATCACCGAAAGGGGACTAACAGGAACTAACAGCTGTAAC 1657

Qy 540 TGATGACCAA 549

Db 1658 CCTTCGGAA 1667

Db 380 GAACTAATTCAGCAGTT 396

RESULT 3

US-09-713-550-150

; Sequence 150, Application US/09713550

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER

; CURRENT APPLICATION NUMBER: US/09/713,550

; FILE REFERENCE: 210121-484C4

; CURRENT FILING DATE: 2000-11-14

; NUMBER OF SEQ ID NOS: 205

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 150

; LENGTH: 396

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-713-550-150

Query Match 23.3%; Score 137; DB 3; Length 396;

Best Local Similarity 100.0%; Pred. No. 1.2e-30;

Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 260 GTTGTCCCTTAATATGGTGCACAGCTTACTGATCACATGAG 120

Db 320 TCCAATGTGCCACCTAACAGAGATACTCAAGCTTACTGATCACATGAG 379

Qy 121 GAACTAATTCAGCAGTT 137

Db 380 GAACTAATTCAGCAGTT 396

RESULT 4

US-09-825-294-150

; Sequence 150, Application US/09825294

; Patent No. 6710170

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Stolk, John A.

; APPLICANT: Algate, Paul A.

; APPLICANT: Fling, Steven P.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER

; CURRENT APPLICATION NUMBER: US/09/825,294

; FILE REFERENCE: 210121-484C5

; CURRENT FILING DATE: 2001-04-03

; NUMBER OF SEQ ID NOS: 215

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 150

; LENGTH: 396

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-825-294-150

Query Match 23.3%; Score 137; DB 3; Length 396;

Best Local Similarity 100.0%; Pred. No. 1.2e-30;

Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 260 GTTGTCCCTTAATATGGTGCACAGCTTACTGATCACATGAG 120

Db 320 TCCAATGTGCCACCTAACAGAGATACTCAAGCTTACTGATCACATGAG 379

Qy 121 GAACTAATTCAGCAGTT 137

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GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: February 20, 2006, 11:17:34 ; Search time 713 Seconds
 (without alignments)

Title: US-10-785-981-3

Perfect score: 589

Sequence: 1 gttgttcctttaatatgt.....tagtccattgaaatccctgg 589

Scoring table: IDENTITY_NUC
 Gapext 1.0

Gapext 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0\$ Maximum Match 100\$

Listing first 45 summaries

Result No.	Score	Query	Match Length	DB ID	Description
1	589	100.0	589	9 US-10-785-981-3	Sequence 3, Appli
2	589	100.0	589	9 US-10-789-723-3	Sequence 3, Appli
3	589	100.0	589	9 US-10-745-237-143	Sequence 3, Appli
4	528.4	89.7	1932	4 US-10-745-237-341	Sequence 341, Appli
5	528.4	89.7	2414	6 US-10-264-237-328	Sequence 528, Appli
6	528.4	89.7	2703	5 US-10-037-270-152	Sequence 152, Appli
7	528.4	89.7	2703	6 US-10-117-722-152	Sequence 152, Appli
8	528.4	89.7	2703	9 US-10-122-851-152	Sequence 152, Appli
9	391.6	66.5	2734	9 US-10-450-763-20426	Sequence 20426, A
10	304	51.6	529	4 US-09-925-065A-278867	Sequence 278867,
11	304	51.6	529	4 US-09-925-065A-278867	Sequence 278867,
12	247	41.9	595	4 US-09-925-065A-278868	Sequence 278868,
13	180.2	30.6	510	3 US-09-783-590-2379	Sequence 2979, Appli
14	137	23.3	396	3 US-09-825-294-150	Sequence 150, Appli
15	137	23.3	396	3 US-09-925-065A-278866	Sequence 150, Appli
16	137	23.3	396	6 US-10-212-677-150	Sequence 150, Appli
17	137	23.3	396	6 US-10-361-811-150	Sequence 150, Appli
18	137	23.3	396	6 US-10-361-811-150	Sequence 150, Appli
19	59.4	10.1	492	3 US-09-918-995-8741	Sequence 8741, Appli
20	59	10.0	1208	9 US-10-450-763-20425	Sequence 20425, A
21	51	8.7	469	9 US-10-785-981-4	Sequence 4, Appli
22	51	8.7	469	9 US-10-789-723-4	Sequence 4, Appli
23	51	8.7	469	9 US-10-786-052-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
 US-10-785-981-3

; Sequence 3, Application US-10785981
 ; Publication No. US20050112597A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GYBONGSANGNM-D0
 ; ATTORNEY OR AGENT NAME: CHULWOO, KIM
 ; TITLE OF INVENTION: SCREENING EXPRESSION PROFILE OF GROWTH SPECIFIC GENES IN SWINE
 ; TITLE OF INVENTION: AND FUNCTIONAL CDNA CHIP PREPARED BY USING THE SAME
 ; FILE REFERENCE: 3884-0120P
 ; CURRENT APPLICATION NUMBER: US-10/785, 981
 ; CURRENT FILING DATE: 2004-06-26
 ; PRIORITY APPLICATION NUMBER: KR 2003-83653
 ; PRIORITY FILING DATE: 2003-11-24
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO: 3
 ; LENGTH: 589
 ; TYPE: DNA
 ; ORGANISM: Kagoshima Berkshire

US-10-785-981-3

Query Match 100.0%; Score 589; DB 9; Length 589;
 Best Local Similarity 100.0%; Pred. No. 7.6e-18;
 Matches 589; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGTTCCTTAATATGATGTTGCCACAGCTGATGGAGCTCATGGCTATT
 Db 1 GTGTTCCTTAATATGATGTTGCCACATGGCTCATGGCTATT
 Qy 1 GTGTTCCTTAATATGATGTTGCCACATGGCTCATGGCTATT
 Db 1 GTGTTCCTTAATATGATGTTGCCACATGGCTCATGGCTATT

61 TCCATGTTCCACCTACAGAGATACTTCAACTTCTTACTGATCTACAGTGAG 120
 61 TCCATGTTCCACCTACAGAGATACTTCAACTTCTTACTGATCTACAGTGAG 120

61 GAAATTCATCAGCAGTCATTGATGTCCTGAGCTGAGTCAGTCAAGAAAGCTGCTCTGTCT 180
 61 GAAATTCATCAGCAGTCATTGATGTCCTGAGCTGAGTCAGTCAAGAAAGCTGCTCTGTCT 180

121 TTACCTAGGTGATGAAACCTGACGAATGAGTTGATGTTGATGAAAGCA 240
 121 TTACCTAGGTGATGAAACCTGACGAATGAGTTGATGTTGATGAAAGCA 240

181 TTACCTAGGTGATGAAACCTGACGAATGAGTTGATGTTGATGAAAGCA 240
 181 TTACCTAGGTGATGAAACCTGACGAATGAGTTGATGTTGATGAAAGCA 240

241 AATGTTGCAATCCCTGTTCTGGGGCATTTGATGAAACCCCTGTGAC 300
 241 AATGTTGCAATCCCTGTTCTGGGGCATTTGATGAAACCCCTGTGAC 300

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OM nucleic - nucleic search, using sw model.

Run on: February 20, 2006, 11:27:30 ; Search time 450.034 Seconds (without alignments)

Title: US-10-785-981-3

Perfect score: 589

Sequence: 1 gttgttccttaatatgtat.....tagccattgaaatccctgg 589

Scoring table: IDENTITY_NUC Gapext 1.0

Searched: 7204323 seqs, 1061406715 residues

Total number of hits satisfying chosen parameters: 14408656

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

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3: /cn2_6/podata/2/pubbra/US06_NEW_PUB.seq;*

4: /cn2_6/podata/2/pubbra/PCT_NEW_PUB.seq;*

5: /cn2_6/podata/2/pubbra/US09_NEW_PUB.seq;*

6: /cn2_6/podata/2/pubbra/US09_NEW_PUB.seq;*

7: /cn2_6/podata/2/pubbra/US10_NEW_PUB.seq;*

8: /cn2_6/podata/2/pubbra/US10_NEW_PUB.seq;*

9: /cn2_6/podata/2/pubbra/US11_NEW_PUB.seq;*

10: /cn2_6/podata/2/pubbra/US11_NEW_PUB.seq;*

11: /cn2_6/podata/2/pubbra/US11_NEW_PUB.seq;*

12: /cn2_6/podata/2/pubbra/US11_NEW_PUB.seq;*

13: /cn2_6/podata/2/pubbra/US60_NEW_PUB.seq;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	304	51.6	529	6	US-09-925-065A-278866
2	304	51.6	529	6	US-09-925-065A-278867
3	247	41.9	595	6	US-09-925-065A-278868
c	4	45	7.6	637	6 US-09-925-065A-754045,
5	43.6	7.4	5925	12	US-11-006-688-1358
6	41.2	7.0	2147	8	US-10-750-185-40169
c	8	39.4	6.7	493	6 US-09-925-065A-301178
c	9	39.4	6.7	493	6 US-09-925-065A-301179
10	37.8	6.4	822	8	US-10-793-626-607
c	11	37.8	6.4	1400	12 US-11-136-527-6340
c	12	37.8	6.4	2950	8 US-10-793-626-3349
c	13	37.8	6.4	3378	12 US-11-136-527-2444
c	14	37.8	6.4	3760	8 US-10-793-626-029
c	15	37.4	6.3	405	6 US-09-925-065A-406315
c	16	37.4	6.3	577	6 US-09-925-065A-474125
c	17	37.4	6.3	618	6 US-09-925-065A-945455
c	18	37.4	6.3	643	6 US-09-925-065A-801427
c	19	37.4	6.3	643	6 US-09-925-065A-801428
c	20	37.4	6.3	643	6 US-09-925-065A-801429

ALIGNMENTS

RESULT 1
US-09-925-065A-278866
; Sequence 278866, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 1038827.135
; CURRENT APPLICATION NUMBER: US/09-925-065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243, 096
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 60/252, 147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250, 092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261, 766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289, 846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 278866
; LENGTH: 529
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-278866
Query Match 51.6%; Score 304; DB 6; Length 529;
Best Local Similarity 100.0%; Pred. No. 1..2e-68;
Matches 304; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OM nucleic - nucleic search, using sw model

Run on: February 20, 2006, 10:36:14 ; Search time 2837,15 Seconds
9396.598 Million cell updates/sec

Title: US-10-785-981-4

Perfect score: 469

Sequence: 1 catttatggggctacgcgc.....tagtgcattgaaatccctgg 469

Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0\$ Maximum Match 10\$ Listing first 45 summaries

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 2: gb_in:/*
 3: gb_env:/*
 4: gb_om:/*
 5: gb_ov:/*
 6: gb_dat:/*
 7: gb_ph:/*
 8: gb_pr:/*
 9: gb_to:/*
 10: gb_sts:/*
 11: gb_sy:/*
 12: gb_un:/*
 13: gb_vl:/*
 14: gb_htg:/*
 15: gb_pl:/*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB ID	Description
1	9	408	2	87.0	1131	CR541796 Homo sapi
2	10	408	2	87.0	1134	AY833990 Synthetic
3	11	408	2	87.0	1374	CQ714735 Sequence
4	12	408	2	87.0	1374	CS119314 Sequence
5	13	408	2	87.0	1381	A8834441 Sequence
6	14	408	2	87.0	1381	AK096902 Homo sapi
7	15	408	2	87.0	1694	BC012597 Homo sapi
8	16	406	6	86.7	1134	CR536516 Homo sapi
9	17	406	6	86.7	1374	HUMACTASK Human adult
10	18	353	2	75.3	1587	AB086240 Coryphaen
11	19	352	2	75.1	1419	MUSASM Mouse skele
12	20	351	6	75.0	1568	AB021652 Coryphaen
13	21	351	6	75.0	1582	AB086242 Coryphaen
14	22	350	4	74.7	1457	BC014877 Mus muscu
15	23	350	4	74.6	1611	AB021650 Coryphaen
16	24	348	8	74.4	1518	BC061974 Rattus no
17	25	347	2	74.0	1251	X03766 Mouse mRNA
18	26	347	2	74.0	2472	AB052654 Lampetra

ALIGNMENTS

RESULT 1						
CR541796	LOCUS	CR541796	Homo sapiens	1131 bp mRNA	PRI 29-JUN-2004	
	DEFINITION		full open reading frame cDNA clone RZPDob834B061ID for gene ACTAI, actin, alpha 1, skeletal muscle; complete cds, without Stopcodon.			
	ACCESSION	CR541796				
	VERSION	CR541796.1	GI:49456548			
	KEYWORDS		Full ORF shuttle clone, Gateway(TM), complete cds.			
	SOURCE		Homo sapiens (human)			
	ORGANISM		Homo sapiens			
	Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Buarchontoglires; Primates; Catarrhini; Hominoidea; Homo.					
	REFERENCE	1 (bases 1 to 1131)				
	AUTHORS	Halleck,A., Ebert,L., Mkoundinya,M., Schick,M., Eisenstein,S., Neubert,P., Kstrang,K., Schatten,R., Shen,B., Henze,S., Mar,W., Korn,B., Zuo,D., Hu,Y. and LaBaer,J.				
	TITLE	Cloning of human full open reading frames in Gateway(TM) system entry vector (pDOI201)				
	JOURNAL	Unpublished				
	COMMENT	2 (bases 1 to 1131)				
	AUTHORS	Halleck,A., Ebert,L., Mkoundinya,M., Schick,M., Eisenstein,S., Neubert,P., Kstrang,K., Schatten,R., Shen,B., Henze,S., Mar,W., Korn,B., Zuo,D., Hu,Y. and LaBaer,J.				
	TITLE	Direct Submission				
	JOURNAL	Submitted (28-JUN-2004) RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH, Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany				
	COMMENT	RZPD; RZPPO834B0631D, ORFNO 3650				
	AUTHORS	Human Full ORF Clones Gateway(TM) - RZPD (kan-resist.) RZPD LIB No. 834				
	TITLE	www.rzpd.de/cgi-bin/products/showLib.pl.cgi/response?libNo=834				
	JOURNAL	www.rzpd.de/cgi-bin/products/orfclones/				
	COMMENT	Contact: Inge Arlart				
	AUTHORS	RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH, Heinrich Heine Strasse 6, D-44059 Berlin, Germany				
	TITLE	Tel: +49 30 32639 100				
	JOURNAL	Fax: +49 30 32639 111				
	COMMENT	www.rzpd.de				

This clone is available from RZPD.
 Contact RZPD (customer.service@rzpd.de) for further information.
 Clone name at Harvard Institute of Proteomics
 (www.hip.harvard.edu/) : FHU130947.01L
 This CDS clone is part of a collection of human full ORF clones
 Jointly established and verified by the Harvard Institute of
 Proteomics (HIP) and RZPD.
 This CDS has been cloned without stopcodon.
 The CDS has been inserted into pDONR201 via a BP Clonase (TM)
 reaction. Additional sequence has been added in front of the start
 codon: att_ AAAAA GCA GGC TCC ACC (ATG) .
 The last codon is followed by the 3' att site: GACCCAGCTTCTTCTT .
 The clone is validated by full sequence check.
 Compared to the reference sequence NM_001100 (GI:5016087) we did
 not find any amino acid exchanges.
 Clone distribution: <http://www.rzpd.de/products/orfclones/>.

FEATURES
 source
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="Taxon:9606"
 /clone_lib="Human Full ORF Clones Gateway (TM) - RZPD"
 /clone_id="RZPD834B0631D"
 /lab_host="DH5Alpha"
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 /translation="MCDEDETALAVCDNGSLVKAAGFAGDDAPRAVPSIVNPRHQQ
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 VTHNPVLYEGALPHAINRLDAGRLDTYKMLLTERGSVTVTAIRIYDIREKL
 CYVALDFNEMATAASSLESLEYSPQVLTIGVTPSPITMESEAGI
 HETTYYNSIMKDIDIRKDLYANNVMSGTTMYPGLIAIDRMOKITALAPSTMKIKIAP
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ORIGIN

Query	Score	Length	Best Local Similarity	Pred.	No.	Mismatches	Indels	Gaps	source	FEATURES
Qy	87.0%	408.2;	DB 8;	Score	1131;					/organism="synthetic construct"
Db	97.9%	424;	Pred.	No.	1..6-58;					/mol_type="mRNA"
Qy	1	CATTATGAGGCTACCTGTAGAATCTCTACTGAGCTGGCTACTCCCTC-TGACCACAC	119							/db_xref="Taxon:32630"
Db	498	CATTATGAGGCTACCTGTAGAATCTCTACTGAGCTGGCTACTCCCTC-TGACCACAC	60							/clone="FHL130947.01L"
Qy	61	TCTTACCGCACTACCTGTAGAATCTCTACTGAGCTGGCTACTCCCTC-TGACCACAC	557							/lab_host="Escherichia coli DH5alpha T1 resistant"
Db	558	TCTTACCGCACTACCTGTAGAATCTCTACTGAGCTGGCTACTCCCTC-TGACCACAC	617							/note="derived from Homo sapiens first strand cDNA library"
Qy	1	CATTATGAGGCTACCTGTAGAATCTCTACTGAGCTGGCTACTCCCTC-TGACCACAC	179							1..>1134
Db	618	TGAGCGCGAGATCGTGGCGGACATCAAGGAGAACCTGCTACGTGGCTACTCCCTC-TGACCACAC	677							/gene="ACTA1"
Qy	180	GAACCGAGATCGAGCTGGCGGACATCAAGGAGAACCTGCTACGTGGCTACTCCCTC-TGACCACAC	239							/note="skeletal muscle"
Db	678	GAACCGAGATCGAGCTGGCGGACATCAAGGAGAACCTGCTACGTGGCTACTCCCTC-TGACCACAC	737							/codon_start=1
Qy	240	CGGGCAGGCTCATCACCATCGGCAACAGAGGCTTCGGCTGCCGAGAACCTCTCCAC	299							/transl_table=11
Db	738	CGGGCAGGCTCATCACCATCGGCAACAGAGGCTTCGGCTGCCGAGAACCTCTCCAC	797							/product="actin alpha 1"
Qy	300	CTCCCTCATCGTGTAGGACTGGCGGGCATTCAGAGCTTCAACAGCATCATGAA	359							/protein_id="AAK37027.1"
Db	798	CTCCCTCATCGTGTAGGACTGGCGGGCATTCAGAGCTTCAACAGCATCATGAA	857							/db_xref="GI:60332848"
Qy	360	GTGTGACATCGACATCGAGGAGGACTGTATGCCAACAGCTATGTCCGGGGACAC	419							/translation="MCDEDETALAVCDNGSLVKAAGFAGDDAPRAVPSIVNPRHQQ VMGMGMQDKDSYVDEAQSKRGILTYKPIERGLITWMDMECKIWHETFYNELRVABEE HPTPLTEAPLNPKANREPMOTOMFETENPVPAVVAQAVLSSYASERTTGIVLDSDNG VTHNPVLYEGALPHAINRLDAGRLDTYKMLLTERGSVTVTAIRIYDIREKL CYVALDFNEMATAASSLESLEYSPQVLTIGVTPSPITMESEAGI HETTYYNSIMKDIDIRKDLYANNVMSGTTMYPGLIAIDRMOKITALAPSTMKIKIAP PERKYSWIGGSIASLSFQQMWIIRQEYDLAGPSIVHRCF"
Db	858	GTGTGACATCGACATCGAGGAGGACTGTATGCCAACAGCTATGTCCGGGGACAC	917							/ORIGIN
Qy	1	CATTATGAGGCTACCTGTAGAATCTCTACTGAGCTGGCTACTCCCTC-TGACCACAC	60							87.0%; Score 408.2; DB 11; Length 1134;
Db	498	CATTATGAGGCTACCTGTAGAATCTCTACTGAGCTGGCTACTCCCTC-TGACCACAC	498							Best Local Similarity 97.9%; Pred. No. 1..6-58;

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OM nucleic - nucleic search, using sw mode!

Run on: February 20, 2006, 10:32:49 ; Search time 398.012 Seconds
 (without alignments)

Title: US-10-785-981-4

Perfect score: 469

Sequence: 1 cattataggggctacgccc.....tagtgccattgtaaatcttgg 469
 7853.391 Million cell updates/sec

Scoring table: IDENTITY NUC
 Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0\$
 Maximum Match 100\$
 Listing first 45 summaries

Database :	N_Geneseq_21: 1: geneseqm1980s: 2: geneseqm1990s: 3: geneseqm2000s: 4: geneseqm2001as: 5: geneseqm2001bs: 6: geneseqm2002as: 7: geneseqm2002bs: 8: geneseqm2003as: 9: geneseqm2003bs: 10: geneseqm2004cs: 11: geneseqm2004bs: 12: geneseqm2004as: 13: geneseqm2004bs: 14: geneseqm2005s: 15: geneseqm2005bs: 16: geneseqm2005as: 17: geneseqm2006as: 18: geneseqm2006bs: 19: geneseqm2007as: 20: geneseqm2007bs: 21: geneseqm2008as: 22: geneseqm2008bs: 23: geneseqm2009as: 24: geneseqm2009bs: 25: geneseqm2010as: 26: geneseqm2010bs: 27: geneseqm2011as: 28: geneseqm2011bs: 29: geneseqm2012as: 30: geneseqm2012bs: 31: geneseqm2013as: 32: geneseqm2013bs: 33: geneseqm2014as: 34: geneseqm2014bs: 35: geneseqm2015as: 36: geneseqm2015bs: 37: geneseqm2016as: 38: geneseqm2016bs: 39: geneseqm2017as: 40: geneseqm2017bs: 41: geneseqm2018as: 42: geneseqm2018bs: 43: geneseqm2019as: 44: geneseqm2019bs: 45: geneseqm2020as: 46: geneseqm2020bs: 47: geneseqm2021as: 48: geneseqm2021bs: 49: geneseqm2022as: 50: 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PA	(ROUJ/)	ROU J.	ID	ADZ79334 standard; cDNA; 469 BP.
PA	(KWAC/)	KWACK S.	XX	ADZ79334;
PA	(CHOI/)	CHOI I.	XX	28-JUL-2005 (first entry)
PA	(KIMB/)	KIM B.	XX	Swine growth factor GF-IV cDNA for cDNA chip diagnostic method.
PI	Kim C,	Yeo J, Lee J, Song Y, Cho K, Chung K, Kim I, Jin S;	XX	
PI	Park S,	Jung J, Lee M, Kwon E, Cho B, Cho H, Shin S, Nam H;	XX	
PI	Hong Y,	Kang Y, Ha Y, Rou J, Kwack S, Choi I., Kim B;	XX	
XX	DR WPI:	2005-403240/41.	XX	biochip; screening; EST; expressed sequence tag; probe; muscle; immobilization; gene expression; polymorphism; diagnosis; animal breeding; growth factor; ss.
PT	Functional cDNA chip useful for screening and function analysis of growth specific genes according to breeds and tissues of swine, comprises substrate and probe comprising growth specific genes in muscle and fat tissues of swine.	XX	XX	Unidentified.
PT	Sequence 469 BP; 106 A; 146 C; 133 G; 84 T; 0 U; 0 Other;	XX	OS	US2005112602-A1.
PS	Claim 2; SEQ ID NO 4; spp; English.	XX	PN	US2005112602-A1.
XX	The invention relates to a functional cDNA chip (I) for screening and function analysis of growth specific genes according to breeds and tissues of swine, comprises a probe comprising growth specific genes in muscle and fat tissues of swine, and a substrate on which the probe is immobilized. Further disclosed is a kit (KI) useful for screening and functional analysis of growth specific gene according to breeds and tissues of swine, comprising (I) integrated in it, Cy5-dCTP or Cy3-dCTP bound cDNA from RNA of the tissue to be screened, a fluorescence scanning system, and a computer analysis system (II) and (KI) are useful for screening and function analysis of growth specific gene according to breeds and tissues of swine. (I) is useful in the swine improvement and breeding of a new breed, and in the hog raising industry. The current sequence represents the pig growth factor IV (GF IV) gene.	XX	XX	
CC	Sequence 469 BP; 106 A; 146 C; 133 G; 84 T; 0 U; 0 Other;	XX	XX	
CC	Query Match 100.0%; Score 469; DB 14; Length 469;	XX	XX	
CC	Best Local Similarity 100.0%; Pred. No. 1-4e-100;	XX	XX	
CC	Matches 469; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	XX	XX	
Qy	1 CATTATGAGGGCTAACGGCCTATGCCAACGCTGGACCTCGCCGAGCGCA 60	XX	XX	
Db	1 CATTATGAGGGCTAACGGCCTAGCGCTGCCAACGCTGGACCTCGCCGAGCGA 60	XX	XX	
Qy	61 TCTTACCGACTACCTGATGAGATACTCTACTGACCAAGCT 120	XX	XX	
Db	61 TCTTACCGACTACCTGATGAGATACTCTACTGACCAAGCT 120	XX	XX	
Qy	121 GAGCGGAGATGTGGCGAGCATCAGGAGAGGTGTGGCTACGTCGGACTCGAG 180	XX	XX	
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Qy	181 AACGAGATGGAGACGCCCTCCCTCCCTGGAAAGAGGTACAGAGTCGAGAC 240	XX	XX	
Db	181 AACGAGATGGAGACGCCCTCCCTCCCTGGAAAGAGGTACAGAGTCGAGAC 240	XX	XX	
Qy	241 GGGCAGTGTACCATGGAAAGGAGCTTGATGCCAACCTCATGTCGGGGACCACT 300	XX	XX	
Db	241 GGGCAGTGTACCATGGAAAGGAGCTTGATGCCAACCTCATGTCGGGGACCACT 300	XX	XX	
Qy	301 TCCTTCATCGGTATGGAGCTGGGGCATTCAGAGACACCTACATGGAGCTGG 360	XX	XX	
Db	301 TCCTTCATCGGTATGGAGCTGGGGCATTCAGAGACACCTACATGGAGCTGG 360	XX	XX	
Qy	361 TGTGACATGACATGGAAAGGAGCTTGATGCCAACCTCATGTCGGGGACCACT 420	XX	XX	
Db	361 TGTGACATGACATGGAAAGGAGCTTGATGCCAACCTCATGTCGGGGACCACT 420	XX	XX	
Qy	421 GATGACCAAGGAGGTGATGCCAACAGATGTGCCATTGAAATCTGG 469	XX	XX	
Db	421 GATGACCAAGGAGGTGATGCCAACAGATGTGCCATTGAAATCTGG 469	XX	XX	
PS	Claim 9; SEQ ID NO 4; 15pp; English.	XX	XX	
CC	The invention relates to a cDNA chip for screening and function analysis of swine genes comprising a probe capable of detecting marker genes specifically expressed in the muscle and fat tissues of swine and a substrate on which the probe is immobilized. The invention also includes a kit for screening and function analysis of swine genes comprising the cDNA chip. The cDNA chip is useful for comparing genetic expression of swine genes, particularly for comparing genetic expression according to swine breeds and tissues, genetic mutation screening, genetic polymorphism interpretation, development of new drugs for disease treatment and disease diagnosis, swine improvement. This sequence corresponds to the cDNA for a growth factor detected using the chip of the invention.	XX	XX	
SQ	Sequence 469 BP; 106 A; 146 C; 133 G; 84 T; 0 U; 0 Other;	XX	XX	

Copyright (c) 1993 - 2006 Biocceleration Ltd.	GenCore version 5.1.7
OM nucleic - nucleic search, using sw model	
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Title:	US-10-785-981-4
Perfect score:	469
Sequence:	1 cattatagggttacgcgc.....tagtgcattgaaatccctgg 469
Scoring table:	IDENTITY NUC Gapop 10.0 , Gapext 1.0
Searched:	41078325 seqs, 23393541228 residues
Total number of hits satisfying chosen parameters:	82156650
Minimum DB seq length:	0
Maximum DB seq length:	2000000000
Post-processing: Minimum Match 0‡ Maximum Match 100‡	Listing first 45 summaries

*
Listing first 45 summaries

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	2: gb_est2:*
	3: gb_est3:*
	4: gb_htc:*
	5: gb_est4:*
	6: gb_est5:*
	7: gb_est6:*
	8: gb_est7:*
	9: gb_gb81:*
	10: gb_gb82:*
	11: gb_gb83:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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- 1	408.2	87.0	483	2	BF826972	RC1-HN003	
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3	408.2	87.0	583	3	BP316694	BP316694	CP552285 AGENCOURT
4	408.2	87.0	872	6	BP493879	BP493879	DR174141 HR0001.C1
5	408	87.0	520	8	DR174141	HR0001.C1	BK199822 DK2P779J
6	406.6	86.7	576	5	BK199822	DK2P779J	BK199822 DK2P779J
7	406.6	86.3	598	3	BP317419	BP317419	CR752996 DK2P468B
8	403.4	86.0	615	4	BP791305	BP791305	CR791305 DK2P468C
9	403.4	86.0	583	7	CN363604	CN363604	CN363604 170006000
10	403.4	86.0	1543	4	CR853327	CR853327	CR853327 Pongo pygmaeus
c 11	403.2	86.0	527	2	BP826015	BP826015	BP826015 MR2-HN003
12	403.2	86.0	581	3	BP319712	BP319712	BP319712 BP319712
13	402.4	85.8	765	7	CR752996	CR752996	CR752996 DK2P468B
c 14	401	85.5	519	6	CB483530	CB483530	CB483530 EST_038 S
c 15	400.2	85.3	686	6	CD610657	CD610657	CD610657 EST_038 S
16	399	85.1	583	3	BP19352	BP19352	BP19352 BP19352
17	392.2	83.6	628	3	BP265037	BP265037	BP265037 BP265037
18	391.2	83.4	532	1	AJ710329	AJ710329	AJ710329 AJ710329
19	385.2	82.9	827	2	BF790986	BF790986	BF790986 602251034
20	384.2	81.9	585	1	AA180732	AA180732	AA180732 AA180732
21	381.8	81.4	634	8	DN413152	DN413152	DN413152 LIB4215-0
22	381	81.2	526	3	BP265026	BP265026	BP265026 BP265026

ALIGNMENTS

RESULT 1	BF826972	463 bp	mRNA	linear	EST 13-JAN-2001
LOCUS	RC1-HN0031-221100-012-h12	HNV031	Homo sapiens	CDNA,	mRNA sequence .
DEFINITION					
ACCESSION	BF826972				
VERSION	BF826972.1	GI:12170455			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eureleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.				
REFERENCE	1 (bases 1 to 483)				
AUTHORS	Dias Neto,E., Garcia Correa,R., Verjovskii-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.P., Matsukuma,A., Baiu,G.S., Simpson,D.H., Brunstein,A., de Oliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J., and Simpson,A.J.				
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)				
PUBLISHED	10/3/800				
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br				
	This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=RC1&t2=RC1-HN0031-221100-012-h12&t3=2000-11-22&t4=1)				
	Seq primer: puc 18 forward High quality sequence stop: 483. Location/Qualifiers				
	1. -483 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /dev_stage="Adult" /clone_id="HN0031" /note="Organ: head_normal; Vector: puci8; Site_1: SmaI;				

Site 2: SmalI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions.^a

ORIGIN

Query Match 87.0%; Score 408.2; DB 2; Length 483;
Best Local Similarity 97.9%; Pred. No. 1.2e-89;
Matches 424; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

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Qy	1 CATTATGAGGTACGGTGGCCATGCCATGGCCTGAACTGGCGCA 60	/organism="Homo sapiens"
Db	51 CATTATGAGGTACGGTGGCCATGCCATGGCCTGAACTGGCGCA 110	/mol type="mRNA"
Qy	61 TCTTACCGACTACCTGATGAAATGCTCATGAGCTTCTCTTC 119	/db_xref="Taxon:9606"
Db	111 TCTTACCGACTACCTGATGAAATGCTCATGAGCTTCTCTTC 170	/dev_stage="Adult"
Qy	120 TGAGCCGAGATCGGCCACATCAGAGAAGTGTGTTACCTGGCC 179	/clone lib=IT0011"
Db	171 TGAGCCGAGATCGGCCACATCAGAGAAGTGTGTTACCTGGCC 230	/note="Organ: epid rumor; Vector: puc18; Site 1: SmalI; site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
Qy	180 GAACGAGATGGCACGGCCGCTCTCCCTGGAAAAGGCTGAGGTGCCAGA 239	Query Match 87.0%; Score 408.2; DB 2; Length 524;
Db	231 GAACGAGATGGCACGGCCGCTCTCCCTGGAAAAGGCTGAGGTGCCAGA 290	Best Local Similarity 97.9%; Pred. No. 1.2e-89;
Qy	240 CGGGCAGGTCACTACCATGGCAACGGGCTTCCGGTGCCTCCAGCC 299	Matches 424; Conservative 0; Mismatches 8; Indels 1; Gaps 1;
Db	291 CGGGCAGGTCACTACCATGGCAACGGGCTTCCGGTGCCTCCAGCC 350	
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Db	351 CTCCCTCATCGGTATGGATGGCTGGGGCAATTACAGAACCTAACAGCTCTGA 410	Db 37 CATTATGAGGTACGGTGGCCATGCCATGGCCTGAACTGGCGCA 96
Qy	360 GTGTGACATCGACATCGAGGAGCCTGATGCCAACAGTCAATGCTGGGGCACMC 419	Qy 61 TCTTACCGACTACCTGATGAAAGTCTCATGAGCTTCTTC 119
Db	411 GTGTGACATCGACATCGAGGAGCCTGATGCCAACAGTCAATGCTGGGGCACMC 470	Db 97 TCTTACCGACTACCTGATGAAAGTCTCATGAGCTTCTTC 156
Qy	420 TGATGACCAAGAG 432	Db 120 TGAGCCGAGATGGCACGGCCATGGCTGAAAGAGCTGAGGTGCCACA 179
Db	471 GATGACCTGG 483	Db 157 TGAGCCGAGATGGCACGGCCATGGCTGAAAGAGCTGAGGTGCCACA 216
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BF769879	BF769879	Db 217 GAACGAGATGGCACGGCCGCTCTCCCTGGAAAAGGCTGAGGTGCCAGA 276
LOCUS	BF769879	Qy 240 CGGGCAGGTCACTACCATGGCAACGGGCTTCCGGTGCCTCCAGCC 299
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ACCESSION	IT0011	Qy 300 CTCCCTCATCGGTATGGACTGGGGCAATTACAGAACCTAACAGCTCTGA 359
VERSION	BF769879	Db 337 CTCCCTCATCGGTATGGACTGGGGCAATTACAGAACCTAACAGCTCTGA 396
KEYWORDS	GI:12117779	Qy 360 GTGTGACATCGACATCGAGGAGCCTGATGCCAACAGTCAATGCTGGGGCACMC 419
SOURCE	EST.	Db 397 GTGTGACATCGACATCGAGGAGCCTGATGCCAACAGTCAATGCTGGGGCACMC 456
ORGANISM	Homo sapiens (human)	
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	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo	
REFERENCE	1 (bases 1 to 524)	
AUTHORS	Dias Neto, E., Garcia Correa, R., Verjovskii-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.P., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Batia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., Ohhare, M.J., Soares, F., Brantani, R.R., Reis, L.P., de Souza, S.J. and Simpson, A.J.U.	Qy 420 TGATGACCAAGAG 432
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)	Db 457 GATGACCTGG 469
PUBMED	10737800	RESULT 3
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil	BP316694 BP316694 Sugano cDNA library, pericardium Homo sapiens cDNA clone
TITLE		DEFINITION BP316694 Sugano cDNA library, pericardium Homo sapiens linear EST 17-SEP-2004
JOURNAL		LOCUS BP316694
PUBMED		VERSION BP316694.1 GI:52245669
COMMENT		KEYWORDS BP316694 EST.
		SOURCE Homo sapiens (human)
		ORGANISM Homo sapiens

Leic - nucleic search, using **bw** model

: February 20, 2006, 11:15:29 ; Search time 115.079 Seconds
 (without alignments)
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US-10-785-981-4

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 Gapct 10_0 , Gapext 1.0

 1303057 seqs, 888780828 residues

number of hits satisfying chosen parameters: 2606114

processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed. And is derived by analysis of the total score distribution.

SUMMARIES

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312	66.5	1288	3 US-09-949-016-4886	Sequence 4886, A
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308.8	65.8	1312	3 US-09-949-016-1850	Sequence 1850, A
308.8	65.8	1330	3 US-09-949-016-3553	Sequence 2, App
307.2	65.5	1919	3 US-09-949-016-3553	Sequence 3553, A
307.2	65.5	2376	3 US-09-976-594-496	Sequence 496, A
307.2	65.5	4143	3 US-09-939-016-345	Sequence 345, A
305.6	65.2	1100	3 US-09-949-016-4538	Sequence 4538, A
305.6	65.2	1128	3 US-09-106-17-15	Sequence 15, App
305.6	65.2	1134	3 US-09-106-17-1	Sequence 1, App
304	64.8	1393	3 US-09-919-172-32	Sequence 32, App
294.4	62.8	1489	3 US-09-976-594-730	Sequence 730, A
294.4	62.8	1793	3 US-10-131-827-8857	Sequence 8857, A
294.4	62.8	1814	3 US-09-949-016-5442	Sequence 5442, A
294.4	62.8	3128	3 US-09-919-039-373	Sequence 373, A
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253.2	54.0	3240	3 US-09-631-022-4	Sequence 4, App
250	53.3	33748	2 US-09-261-206A-76	Sequence 76, App
249	53.1	5643	2 US-08-14-02B-4	Sequence 4, App
243.2	51.9	1481	3 US-09-533-559-7	Sequence 7, App
238.8	50.9	2994	3 US-09-153-737A-3	GENERAL_INFO

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RESULT 2
 US-09-949-016-4886
 Patent No. 6912319 Application US/0949016

GENERAL INFORMATION:
 APPLICANT: McHugh, Kirk M.
 TITLE OF INVENTION: DIAGNOSTIC TEST FOR DETERMINING
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
 ADDRESS: No. 5710003ris
 STREET: One Liberty Place - 46th Floor
 CITY: Philadelphia
 STATE: PA
 COUNTRY: USA
 ZIP: 19103

COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/588,113
 FILING DATE:
 CLASSIFICATION: 436

ATTORNEY/AGENT INFORMATION:
 NAME: Ralph, Rebecca L.
 REGISTRATION NUMBER: 35,152
 REFERENCE DOCKET NUMBER: TUU-1652
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 215-568-3100
 TELEFAX: 215-568-3439
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1275 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 55..1186
 US-08/588-113-1

Query Match 66.5%; Score 312; DB 3; Length 1288;
 Best Local Similarity 85.5%; Pred. No. 1.3e-68;
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Qy 180 GAACGAGATGCGACCGCGCTCCCTCTCCCTGAAAGAGCTAACAGTGGCA 239
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 Qy 300 CTCCTCATGCTATGGATTGGACTGGGGCATTCAGAGAACCTAACAGCATGAA 359
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RESULT 3
 US-09-588-113-1
 Sequence 1, Application US/08588113
 Patent No. 5710003

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OM nucleic - nucleic search, using sw model

Run on: February 20, 2006, 11:17:34 ; Search time 567.737 Seconds
 (without alignments)

6831.225 Million cell updates/sec

Title: US-10-785-981-4

Perfect score: 469

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Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing First 45 summaries

RESULT 1
 US-10-785-981-4

; Sequence 4, Application US/10785981
 ; Publication No. US20050112597A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CHULWOOK, KIM
 ; TITLE OF INVENTION: SCREENING EXPRESSION PROFILE OF GROWTH SPECIFIC GENES IN SWINE
 ; TITLE OF INVENTION: AND FUNCTIONAL CDNA CHIP PREPARED BY USING THE SAME
 ; FILE REFERENCE: 3884-0120P
 ; CURRENT APPLICATION NUMBER: US/10-785,981
 ; CURRENT FILING DATE: 2004-06-26
 ; PRIORITY APPLICATION NUMBER: KR 2003-83653
 ; PRIORITY FILING DATE: 2003-11-24
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 4
 ; LENGTH: 469
 ; TYPE: DNA
 ; ORGANISM: Kagoshima Berkshire

US-10-785-981-4

Query Match 100.0%; Score 469; DB 9; Length 469;
 Best Local Similarity 100.0%; Pred. No. 2e-128;
 Matches 469; Conservative 0; Indels 0; Gaps 0;

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	359.9	76.5	461	3 US-09-950-352-14429	Sequence 14429, A
7	350.4	74.7	1446	9 US-10-764-420-5	Sequence 5, Appli
8	312.7	74.0	1134	7 US-10-191-803-116	Sequence 116, APP
9	325.2	69.3	1361	6 US-10-388-934-560	Sequence 560, APP
10	32.2	69.3	1780	9 US-10-764-420-48	Sequence 48, APP
11	312	66.5	1288	6 US-10-341-434-100	Sequence 100, APP
12	312	66.5	1288	6 US-10-172-118-638	Sequence 638, APP
13	312	66.5	1288	7 US-10-342-887-638	Sequence 638, APP
14	312	66.5	1288	9 US-10-923-035-17	Sequence 17, APP
15	308.8	65.8	1330	3 US-09-969-708-62	Sequence 62, APP
16	308.8	65.8	1330	3 US-09-873-367C-811	Sequence 811, APP
17	308.8	65.8	1330	6 US-10-236-031B-63	Sequence 63, APP
18	308.8	65.8	1330	8 US-10-370-715B-231	Sequence 231, APP
19	308.8	65.8	1330	9 US-10-843-641A-811	Sequence 811, APP
20	308.8	65.8	1330	9 US-10-843-641A-7533	Sequence 7533, AP
21	308.8	65.8	1948	5 US-10-198-846-11901	Sequence 11901, A
22	307.4	65.5	501	3 US-09-833-790-158	Sequence 158, APP
23	307.2	65.5	1400	9 US-10-956-157-5886	Sequence 5886, APP

ALIGNMENTS

Database : GenEmbl:*

ALIGNMENTS

RESULT 1
 AX55393/C
LOCUS AX55393 Sequence 5263 from Patent WO03000898.
DEFINITION AX55393
ACCESSION AX55393
VERSION 1
KEYWORDS G1:29158207
SOURCE Oryza sativa
ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1
 Chang, H.S., Chen, W., Cooper, B., Glazebrook, J., Goff, S.A., Hou, Y.M.,
AUTHORS

Katagiri, F., Quan, S., Tao, Y., Whitham, S., Xie, Z., Zhu, T. and Zou, G.
 Plant genes involved in defense against pathogens
 Patent: WO 03000898-A 5263 03-JAN-2003;
 Syngenta Participations AG (CH)
 Location/Qualifiers
 1. .2000

/organism="Oryza sativa"
/mol_type="unassigned DNA"
/Ab_Zref_nr=45700

ORIGIN / www_nerl_cornell_edu

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Query Match      Score 42.4; DB 6; Length 2000;
Best Local Similarity 8.4%; Pred. No. 0.44;

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Matches 40; Conservative 161; Mismatches 157; Indels 0; Gaps 0;

Qy 206 CACCTTACAGGCCACTTTAAAGTTACATCCAGGGCTCTGTACACCCCTAACGGAGT 265

Db 389 MTMYYAYSMMTTWYYAKWYKVRGTMWSYCKSKSYKKVYCTWWCTMKCMRRCYRWR 330

Qy	266	GGAGTGGAGCCGCTTACCGAGTCAGTGCTGCTAG	325
Db	329	KMVKRKTKISKRCYCWRYATCYWCCCYCRKGWSRMRMRTAGKWMRSNSRWCRSYW	270

RESULT 2

DROSOPHILAE/C

LOCUS DROSOPHILAE/C

DEFINITION Drosophila melanogaster serendipity (sry h-1) gene, complete cds.

VERSION M23391

KEYWORD DNA-binding protein; multifingered protein gene.

SOURCE Drosophila melanogaster

ORGANISM Drosophila melanogaster

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydriodea; Drosophilidae; Drosophila.

REFERENCE 1. (bases 1 to 4001)

AUTHORS Vincent, A., Kejzarova-Lepesant,J., Segalat,L., Yanicosab,C. and Lepesant,J.A.

TITLE sry h-1, a new Drosophila melanogaster multifingered protein gene showing maternal and zygotic expression

JOURNAL Mol. Cell. Biol. 8 (10), 4459-4468 (1988)

PUBLMED 3141791

COMMENT Original source text: Drosophila melanogaster (strain Canton S) (library: Lauer and Maniatis) DNA.

FEATURES Location/Qualifiers

1. 4001

/organism="Drosophila melanogaster"

/mol_type="genomic DNA"

/strain="Canton S"

/db_xref="taxon:7227"

/map="region 98EF"

/tissue_liber="Lauer and Maniatis"

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mRNA /gene="mRNA including exon 1a"

exon 399..1661

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/note="version a of exon 1"

/number=1

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/note="version b of exon 1"

/number=1

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/standard_name="serendipity"

exon /codon_start=1

/product="DNA-binding protein"

/protein_id="AA28487_1"

/db_xref="GI:387593"

/translation="MEGGKGEGRMKKEAPSKKLPPKTYGGDAGTPKAHHBILSSL

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KVECVSEELLPSTF1FQQAASSAESDRLACRPASETPLEVDAPLHKCLDCNL
CGKCLKLGSMMMRKHSNDNPKYOCSDICGOKFVKQNLTHARHINSEKPYCPECOK
REFERSHLQRQKHYAOTSRSCIECKGKMYTIERCLKVHNVLHSLQRPFACTVCDKSF
CSKSKPTTNKACKAAAAAAAASAYVNPNELASSELAKARANLTTESTAAPAKQK
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RKQLAPRQLQQRPLQHQGQPOQSSUBP PAVPQIKKEPVQGPFLDLHGJLTSABE
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PCKPSDRILACPSLESSPSSPASMLETTAVSCASSVAISTNALPVSGNLYLPAPLNA
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/number=1

exon 1722..2926
/gene=sry h-1"
/number=2

intron 2927..3036
/gene=sry h-1"
/number=2

exon 3037..3751
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/number=3

polyA_signal 3728..3733
/gene=sry h-1"

ORIGIN

Query Match 8.2%; Score 41.4%; DB 2; Length 4001;
Best Local Similarity 54.2%; Prod. No. 0..89; Indels 0; Gaps 0;
Matches 84; Conservative 0; Mismatches 71;

Qy 258 TAAGCACTGGCAGTGATGCCGTGCTGGCAGTGTTGGTAGCTCG 317
Db 1345 TAAAGATGGGGAGTAGCTCACCTGACACTGCTACCTGTCCTGCTCG 1286

Qy 318 TCCTAAGCTTCCCGATAGCCGCTTACACCATCGCGGACTAGAACCTGCTG 377
Db 1285 GCGGATGCTTCCTCGGGGCGCTCTGGAGTACCTGTCACCTGAC 1226

Qy 378 GTTGAGCTAAGCTTATGGTAGCAGTGCGCC 412
Db 1225 CCGGCAAGCTTGGCTTGCAGCTGAGTCAGTCAG 1191

RESULT 3

CP000095_06

WCOMMENT

Sequence split into 19 fragments LOCUS CP000095 Accession CP000095

Fragment	Name	Begin	End
CP000095_00		1	110000
CP000095_01		100001	210000
CP000095_02		200001	310000
CP000095_03		300001	410000
CP000095_04		400001	510000
CP000095_05		500001	610000
CP000095_06		600001	710000
CP000095_07		700001	810000
CP000095_08		800001	910000
CP000095_09		900001	1010000
CP000095_10		1000001	1110000
CP000095_11		1100001	1210000
CP000095_12		1200001	1310000
CP000095_13		1300001	1410000
CP000095_14		1400001	1510000
CP000095_15		1500001	1610000

CDS Continuation (7 of 19) of CP000095 from base 600001 (CP000095 Prochlorococcus marinus st

Result No.	Score	Query Match	Length	DB ID	Description
1	507	100.0	507	14 ADZ89042	Adz89042 Pig growth factor I (GF V) gene, seq id 5.
2	507	100.0	507	14 ADZ79335	Adz79335 Swine growth factor I (GF V) gene, seq id 5.
3	507	100.0	507	14 ADZ77172	Adz77172 Pig growth factor I (GF V) gene, seq id 5.
C 4	42.4	8.4	2000	8 ADA71938	Aza00100 Rice Gene
C 5	41.4	8.2	336	2 AAZ00010	Aax88092 Synthetic
C 6	41.4	8.2	336	2 AAX88092	Acl30038 Rice abiotic stress response protein
C 7	40.8	8.0	891	11 ACI30038	Aax88093 Synthetic
JIN S.	8	7.9	336	2 AAX88093	Abl02625 Drosophila
C 9	39.8	7.9	2852	4 ABL02625	Abk92192 Prostate cancer gene
C 10	39.8	7.9	5023	4 ABL02624	Abk92193 Human prostatic
C 11	39.6	7.8	1167	6 ABK53133	Abk92194 Listeria
C 12	39.6	7.8	5643	6 ACA36793	Abq67800 Novel hum
C 13	37.2	7.3	2712	8 ADQ70741	Abq67800 Novel hum
C 14	37.2	7.3	110000	6 ABQ70741	Abq67800 Novel hum
C 15	36.8	7.3	362	14 ADV77137	Abq67800 Novel hum
C 16	36.8	7.3	204803	12 ADQ97348	Abq67800 Novel hum
C 17	36	7.1	728	6 ABQ68881	Abq67800 Novel hum
C 18	36	7.1	1296	6 ABQ67797	Abq67800 Novel hum
C 19	36	7.1	1311	6 ABQ67800	Abq67800 Novel hum

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OM nucleic - nucleic search, using bw model

Run on: February 20, 2006, 10:32:49 ; Search time 430.26 Seconds

Title: US-10-785-981-5
Perfect score: 507

Sequence: 1 tataatagaaccgaaatccatcggtttcagccggcg 507

Scoring table: IDENTITY NUC Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_21:*

1: geneseqn1980s;*
2: geneseqn1990s;*
3: geneseqn2000s;*
4: geneseqn2001as;*
5: geneseqn2001bs;*
6: geneseqn2002as;*
7: geneseqn2002bs;*
8: geneseqn2003as;*
9: geneseqn2003bs;*
10: geneseqn2003cs;*
11: geneseqn2003ds;*
12: geneseqn2004as;*
13: geneseqn2004bs;*
14: geneseqn2005s;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

RESULT 1	XX	ADZ89042 standard; DNA; 507 BP.
ID	XX	ADZ89042;
AC	XX	DT 28-JUL-2005 (first entry)
XX	XX	DE Pig growth factor I (GF V) gene, seq id 5.
XX	XX	KW Growth; biochip; swine; hog raising; growth factor V; gene; ds.
XX	XX	OS Sub scrofa; Kagoshima Berkshire.
XX	XX	PN US2005112597-A1.
XX	XX	PD 26-MAY-2005.
XX	XX	PF 26-FEB-2004; 2004US-00785981.
PR	XX	PR 24-NOV-2003; 2003KR-00083653.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
PA	507	100.0	507	14 ADZ89042	Adz89042 Pig growth factor I (GF V) gene, seq id 5.
PA	507	100.0	507	14 ADZ79335	Adz79335 Swine growth factor I (GF V) gene, seq id 5.
PA	507	100.0	507	14 ADZ77172	Adz77172 Pig growth factor I (GF V) gene, seq id 5.
C 4	42.4	8.4	2000	8 ADA71938	Aza00100 Rice Gene
C 5	41.4	8.2	336	2 AAZ00010	Aax88092 Synthetic
C 6	41.4	8.2	336	2 AAX88092	Acl30038 Rice abiotic stress response protein
C 7	40.8	8.0	891	11 ACI30038	Aax88093 Synthetic
JIN S.	8	7.9	336	2 AAX88093	Abl02625 Drosophila
C 9	39.8	7.9	2852	4 ABL02625	Abk92192 Prostate cancer gene
C 10	39.8	7.9	5023	4 ABL02624	Abk92193 Human prostate
C 11	39.6	7.8	1167	6 ABK53133	Abk92194 Listeria
C 12	39.6	7.8	5643	6 ACA36793	Abq67800 Novel hum
C 13	37.2	7.3	2712	8 ADQ70741	Abq67800 Novel hum
C 14	37.2	7.3	110000	6 ABQ70741	Abq67800 Novel hum
C 15	36.8	7.3	362	14 ADV77137	Abq67800 Novel hum
C 16	36.8	7.3	204803	12 ADQ97348	Abq67800 Novel hum
C 17	36	7.1	728	6 ABQ68881	Abq67800 Novel hum
C 18	36	7.1	1296	6 ABQ67797	Abq67800 Novel hum
C 19	36	7.1	1311	6 ABQ67800	Abq67800 Novel hum

PA (ROU/) ROU J.
 PA (KWAC/) KWACK S.
 PA (CROI/) CHOI I.
 PA (KIMB/) KIM B.
 XX Kim C., Yeo J., Lee J., Song Y., Cho K., Chung K., Kim I., Jin S.;
 Park S., Jung J., Lee M., Kwon E., Cho E., Shin S., Nam H.;
 PI Hong Y., Kang S., Ha Y., Rou J., Kwack S., Choi I., Kim B.;
 XX DR WPI: 2005-403340/41.

XX Functional cDNA chip useful for screening and function analysis of growth specific genes according to breeds and tissues of swine, comprises substrate and probe comprising growth specific genes in muscle and fat tissues of swine.
 XX DR WPI: 2005-403340/41.

XX The invention relates to a functional cDNA chip (I) for screening and function analysis of growth specific genes according to breeds and tissues of swine, comprises a probe comprising growth specific gene in muscle and fat tissues of swine, and a substrate on which the probe is immobilized. Further disclosed is a kit (K1) useful for screening and functional analysis of growth specific gene according to breeds and tissues of swine, comprising (I) integrated in it, Cys-dCTP or Cy3-dCTP bound cDNA from RNA of the tissue to be screened, a fluorescence scanning system, and a computer analysis system. (I) and (K1) are useful for screening and function analysis of growth specific gene according to breeds and tissues of swine. (I) is useful in the swine improvement and breeding of a new breed, and in the hog raising industry. The current sequence represents the pig growth factor V (GF V) gene.
 XX Sequence 507 BP; 117 A; 160 C; 120 G; 110 T; 0 U; 0 Other; Score 507; Length 507; Best Local Similarity 100.0%; Pred. No. 9 1e-153; Length 507; Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TATATAGAACCGAATTACCTTAACTCTGGCCCTGACCAAGGAGGGCAAAACAAGGCCAAACCT 60
 Db 1 TATATAGAACCGAATTACCTTAACTCTGGCCCTGACCAAGGAGGGCAAAACAAGGCCAAACCT 60
 Qy 61 AGGAGGTATAATAGGTATACTGGCGCTGACACATACTACACTACCCGAACGCC 120
 Db 61 AGGAGGTATAATAGGTATACTGGCGCTGACACATACTACACTACCCGAACGCC 120
 Qy 121 GGACAACTAAGGGCTCCGCATAAGCCATTCTCTGGTGTGATGTTGCGGGCTGAG 180
 Db 121 GGACAACTAAGGCCTGGCATAGCCATTCTCTGGTGTGATGTTGCGGGCTGAG 180
 Qy 181 TTATAGGCCGCCAACGGCTATACACCTTACCGCCACTTAACTACATCCAGA 240
 Db 181 TTATAGGCCGCCAACGGCTATACACCTTACCGCCACTTAACTACATCCAGA 240
 Qy 241 GGGCTGTGACACCCCTAACGATGGCAGTGTGACCTGCGCTTACCCCTGGCGAG 300
 Db 241 GGGCTGTGACACCCCTAACGATGGCAGTGTGACCTGCGCTTACCCCTGGCGAG 300
 Qy 361 CGGACTGAGACACCGTTGGTTCAGCTTAAGCTTCCCGATAGCGCGCTTTAGCTGCGCG 420
 Db 361 CGGACTGAGACACCGTTGGTTCAGCTTAAGCTTCCCGATAGCGCGCTTTAGCTGCGCG 420
 Qy 421 TGTAGCCAGCTTACATGTTAGTGTAGCTTACCCCTGGCAATACCGTGTCTCCCTA 480
 Db 421 TGTAGCCAGCTTACATGTTAGTGTAGCTTACCCCTGGCAATACCGTGTCTCCCTA 480
 Qy 481 CTCCAACCTCTCGTTTACGCCGAG 507
 Db 481 CTCCAACCTCTCGTTTACGCCGAG 507

RESULT 2
 AD279335 standard; cDNA; 507 BP.
 ID AD279335;
 AC XX
 DT 28-JUL-2005 (first entry)
 XX Swine growth factor GF-V cDNA for cDNA chip diagnostic method.
 DE XX
 KW biochip; screening; EST; expressed sequence tag; probe; muscle; immobilization; gene expression; polymorphism; diagnosis; animal breeding; growth factor; 95.
 KW XX
 PR Unidentified.
 OS XX
 PN US2005112602-A1.
 PD 26-MAY-2005.
 PR 27-FEB-2004; 2004US-00789723.
 PR 24-NOV-2003; 2003KR-000983651.
 XX (KIMC/) KIM C.
 PA (YEJU/) YEO J.
 PA (LEEW/) LEE J.
 PA (SONG/) SONG Y.
 PA (CRHK/) CHO K.
 PA (CHUN/) CHUNG K.
 PA (KIMI/) KIM I.
 PA (JINS/) JIN S.
 PA (PARK/) PARK S.
 PA (JUNG/) JUNG J.
 PA (LEEM/) LEE M.
 PA (KWN/) KWON E.
 PA (CHOE/) CHOI E.
 PA (CHOH/) CHO H.
 PA (SHIN/) SHIN S.
 PA (NAMH/) NAM H.
 PA (HONG/) HONG Y.
 PA (HONG/) HONG S.
 PA (KANG/) KANG Y.
 PA (HAWY/) HA Y.
 PA (ROU/) ROU J.
 PA (KWAQ/) KWACK S.
 PA (CHOI/) CHOI I..
 PA (KIMB/) KIM B.
 XX DR WPI: 2005-371656/38.
 PT New cDNA chip comprising a probe capable of detecting marker genes specifically expressed in the muscle and fat tissues of swine, and a substrate, useful for screening and function analysis of swine genes.
 PT XX
 PR Claim 9; SEQ ID NO 5; 15pp; English.
 CC The invention relates to a cDNA chip for screening and function analysis of swine genes comprising a probe capable of detecting marker genes specifically expressed in the muscle and fat tissues of swine and a substrate on which the probe is immobilized. The invention also includes a kit for screening and function analysis of swine genes comprising the cDNA chip. The cDNA chip is useful for screening and function analysis of swine genes, particularly for comparing genetic expression according to swine breeds and tissues; genetic mutation screening, genetic polymorphism interpretation, development of new drugs for disease treatment and disease diagnosis, swine improvement. This sequence

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OM nucleic - nucleic search, using sw model

Run on: February 20, 2006, 10:51:20 ; Search time 3003.91 Seconds
(without alignments)

Title: US-10-785-981-5
Perfect score: 507
Sequence: 1 tataatagaacccaaatcacgt.....tcttgtcggtttcagccgag 507

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4107835 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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	5: gb_est4:*
	6: gb_est5:*
	7: gb_est6:*
	8: gb_est7:*
	9: gb_gss1:*
	10: gb_gss2:*
	11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	61	12.0	932	5	BX432596	BX432596	AV429458
c 2	41.4	8.2	529	1	AV429458	AV429458	CJ019297
c 3	41.2	8.1	670	7	CJ019297	CJ019297	BP169281
c 4	41.2	8.1	701	3	BP169281	BP169281	CJ016021
c 5	41.2	8.1	707	7	CJ016021	CJ016021	BP144350
c 6	41.2	8.1	794	3	BP144350	BP144350	DN106813
c 7	41.2	8.1	803	8	DN106813	DN106813	BP156807
c 8	41.2	8.1	810	3	BP156807	BP156807	CJ014151
c 9	41.2	8.1	862	7	CJ014151	CJ014151	DN107179
c 10	41.2	8.1	883	8	DN107179	DN107179	CC086053
c 11	41.2	8.1	896	9	CC086053	CC086053	CSU-K333r
c 12	40.8	8.0	1180	8	DN703457	DN703457	DN703457
c 13	40.2	7.9	649	1	AU296640	AU296640	CO448190
c 14	40.2	7.9	813	7	CO448190	CO448190	BW964713
c 15	39.6	7.8	644	5	BW964713	BW964713	BP153784
c 16	39.6	7.8	692	3	BP153784	BP153784	CP076027
c 17	39.4	7.8	689	6	CP076027	CP076027	Hd_mx17_6
c 18	39.2	7.7	490	7	C0975370	C0975370	C0975370
c 19	39.2	7.7	536	7	C0974837	C0974837	C0974837
c 20	39.2	7.7	567	7	C0972208	C0972208	CN868859
c 21	39.2	7.7	578	7	CN868859	CN868859	CO451557
c 22	39.2	7.7	907	7	CO451557	CO451557	MZCCL1016

RESULT 1

BX432596

LOCUS

BX432596 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone CS00D032YF14

DEFINITION

3-PRIME, mRNA sequence.

ACCESSION

BX432596

VERSION

BX432596.1

EST.

KEYWORDS

Homo sapiens (human)

SOURCE

Homo sapiens

ORGANISM

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominoidea; Hominoidea

Homidae

Human

Genome

Genoscope

Centre National de Séquençage

2 rue Gaston Crémieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: www.genoscope.cns.fr

Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the PCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitrogen.

This sequence belongs to sequence cluster 3874.

For more information about this cluster, see <http://www.genoscope.cns.fr/cna?sc=CSOBH0092B10NP1&c=3874>.

COMMENT

REFERENCE

1 (bases 1 to 932)

AUTHORS

Li W.B., Gruber C., Jesse J. and Polayes D.

TITLE

Full-length cDNA libraries and normalization

JOURNAL

Unpublished (2001)

COMMENT

Contact: Genoscope

Genoscope - Centre National de Séquençage

2 rue Gaston Crémieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: www.genoscope.cns.fr

Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the PCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitrogen.

This sequence belongs to sequence cluster 3874.

r

For more information about this cluster, see <http://www.genoscope.cns.fr/cna?sc=CSOBH0092B10NP1&c=3874>.

Location/Qualifiers

1..932

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/mol type="mRNA"

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/tissue type="FETAL BRAIN"

/dev_stage="fetal"

/clone_id="Homo Sapiens FETAL BRAIN"

/note="Organ: brain; Vector: PCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the PCMVSPORT 6 vector. Library was not normalized."

vector. Library was not normalized."

vector. Library was not normalized."

ALIGNMENTS

Query Match	Score 61; DB 5; Length 932;	QY	
Best Local Matches	48.8%; Pred. No. 3.8e-07; Mismatches 13; Indels 3; Gaps 2;	DB	
2D	130 GGCTCCGCCATAAGCCATCCRITCNCATCGCATGATGCGCTTACGGCTTACAGTCATTAGGC 189	QY	
Db	563 GGGACCGCTATGCCGCCAACCTAGACGATGTGAAGCAGGGCTGATATGAGC 622	DB	358 CGGCGACTAGACCCCTGGTGAACGGTAAGCTATGGTAGAGCTGGGACCG 417
2Y	190 TGCACAAACGCCATACACAGCTTACCAAGCACTATTAAAGTTACATCCACAGGGCTCTGT 249	QY	
Db	623 AGCCTTCGGCCTATCACTCAATTCTGCCTCAACACTGAATATACCTCTGTAGGACAGA 682	DB	218 CGGAGCGGTACCECCCAGATGCGTCAGGGAGCTGGCGCGCGCTGGCGCCG 159
2y	250 ACCACCCCTAAGCTTAACTGGCTAGCTGCTGGCTCCCGTATCCCTGGCACTGTGTGTC 309	RESULT 3	
Db	683 TCCTCCCTCTTCTTCTGAGGTTGAGATGGCGAACGGCAAGAGAGC 742	CJ019297/C	CJ019297 full-length enriched swine cDNA library, adult spleen Sus scrofa cDNA clone SP01C010070 5', mRNA sequence.
2y	310 TAGETCCCTCTTAAGCTTCCCGATAGCGCCGCTTTCACACCATCGCCGGACTAGA 369	LOCUS	
Db	743 ATGAGGACCATTTGCAUTCCCTATGCGCCCAAATCTPTCATAGCGGCCAGCT 802	DEFINITION	
2Y	370 CACCGTGTGGTTGCAAGCTCTATGTTAGCAGCTGCGGACGCCGCTGTAGCCAG 429	ACCESSION	CJ019297
Db	803 ATCCGAGGCCACCTGCGATACGATWTA_GTATCTGTGCCCCGTCGAAAGCCYGC 861	VERSION	CJ019297.1
2y	430 CTTACTATGTTAGTTTCAAGGACCACTCTGCCAATACCCGTTCTACTCCAACTC 489	KEYWORDS	GI:54521136
Db	862 AWAY--CCTWGATGCAAWCCYKCCYTCAGCTTCKSGHGDTCCTCATMCCTTATIC 919	SOURCE	Sus scrofa (pig)
2Y	490 TGTCGGGTTCTAGC 502	ORGANISM	Sus scrofa
Db	920 TGTTGGCTWTGGC 932	COMMENT	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.
2Y	AV429458	REFERENCE	1. (bases 1 to 670) Uenishi, H., Eguchi, T., Suzuki, K., Sawazaki, T., Toki, D., Shinkai, H., Okumura, N., Hamasima, N. and Awata, T.
Db	AV429458_Porphyra_yezoensis_TU-1	AUTHORS	PEDE (pig EST Data Explorer); construction of a database for ESTs derived from porcine full-length cDNA libraries
2Y	PL003403_x 5'	TITLE	Nucleic Acids Res. 32 (1), D484-D488 (2004)
Db		JOURNAL	
2Y	AV429458	PUBLMED	14681463
Db	PL003403_x 5'	COMMENT	Contact: Hirohide Uenishi Animal Genome Laboratory, Genome Research Department National Institute of Agrobiological Sciences 2 Ikenoda, Tsukuba, Ibaraki 305-8602, Japan Tel: +81-29-838-8627 Fax: +81-29-838-8627 Email: huenishi@affrc.go.jp
2Y	AV429458	FEATURES	EST project with full-length enriched cDNA libraries carried out in Animal Genome Research Program (Japan) by National Institute of Agrobiological Sciences and STAFF-Institute Single pass sequencing of clones derived from oligo-capped cDNA library Vector sequences were eliminated by RepeatMasker version 2002/07/13 and crossmatch version 0.990319 Low quality bases were trimmed based on the quality values.
Db	AV429458_V1	source	Location/Qualifiers 1. 670
2Y	AV429458_V1	source	/mol type="Sus scrofa" /mol type="mRNA" /db_xref="taxon:9823" /clone="SP01C010070" /tissue type="spleen" /dev_stage="adult" /clone_lib="full-length enriched swine cDNA library, adult spleen"
Db	10907854	ORIGIN	Query Match Score 41.2; DB 7; Length 670; Best Local Similarity 48.3%; Pred. No. 0.39; Gaps 0;
2Y	1. .523	COMMENT	The First Laboratory for Plant Gene Research Kazusa DNA Research Institute Yana 1532-3, Kisarazu, Chiba 292-0812, Japan Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/
Db	/organism="Porphyra yezoensis"	FEATURES	
2Y	/mol type="mRNA"	source	
Db	/strain="TU-1"	source	
2Y	/db_xref="taxon:2788"	source	
Db	/clone="PL003403_x"	source	
2Y	/clone_lib="Porphyra yezoensis TU-1"	source	
Db	/note="#vector: pBlueScriptII SK; Site_1: EcoRI; Site_2: xhoI"	source	
2Y	322 AAGCTTCCCGATAAGCTTACACCACTCGGACTAGACCCGTTAGCTCCGCTCT 321	ORIGIN	
Db	588 CCGCTGCCTCGGGCTCGAAGCTTGTTGCTGGGGCTGGGGCTGGGGCTGGGG 589	Query Match Score 41.4; DB 1; Length 529;	
2Y	58.5%; Pred. No. 0.32; Mismatches 51; Indels 0; Gaps 0;	Best Local Similarity 8.2%; Pred. No. 0.39; Gaps 0;	
Db	Matches 72; Conservative	Matches 115; Conservative	

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OM nucleic - nucleic search, using sw model

Run on: February 20, 2006, 11:15:29 ; Search time 124.404 Seconds
 7244.353 Million cell updates/sec

Title: US-10-785-981-5
 Perfect score: 507

Sequence: 1 tataatagaaccgaaatcacgt.....tctgtcggtttcagccggag 507

Scoring table: IDENTITY_NUC
 Gapov 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued Patents NA:
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 2: /cn2_6/.ptodata/1/ina/5_COMB.seq:/*
 3: /cn2_6/.ptodata/1/ina/6A_COMB.seq:/*
 4: /cn2_6/.ptodata/1/ina/H_COMB.seq:/*
 5: /cn2_6/.ptodata/1/ina/PCTUS_COMB.seq:/*
 6: /cn2_6/.ptodata/1/ina/PP_COMB.seq:/*
 7: /cn2_6/.ptodata/1/ina/RE_COMB.seq:/*
 8: /cn2_6/.ptodata/1/ina/RE_COMB.seq:/*
 9: /cn2_6/.ptodata/1/ina/backfile1.seq:/*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 1	41.4	8.2	336	2 US-07-814-220-3	Sequence 3, Appli
C 2	41.4	8.2	336	2 US-07-812-421-3	Sequence 3, Appli
C 3	39.8	7.9	336	2 US-07-814-220-4	Sequence 4, Appli
C 4	39.8	7.9	336	2 US-07-812-421-4	Sequence 4, Appli
C 5	39	7.7	7218	2 US-08-232-463-14	Sequence 14, Appli
C 6	7.1	4403765	3	US-09-103-840A-2	Sequence 2, Appli
C 7	34.8	6.9	4411529	3 US-09-103-840A-1	Sequence 1, Appli
C 8	34.6	6.8	336	2 US-07-814-220-3	Sequence 3, Appli
C 9	34.6	6.8	336	2 US-07-812-421-3	Sequence 4, Appli
C 10	34	6.7	1879	2 US-08-403-852D-5	Sequence 5, Appli
C 11	34	6.7	1879	3 US-08-510-646B-5	Sequence 5, Appli
C 12	34	6.7	1879	3 US-09-231-818-5	Sequence 5, Appli
C 13	34	6.7	1879	3 US-09-635-359B-5	Sequence 5, Appli
C 14	33.8	6.7	1294	3 US-09-312-038-4	Sequence 4, Appli
C 15	33.8	6.7	1294	3 US-09-850-964-4	Sequence 4, Appli
C 16	33.8	6.7	2289	3 US-09-312-038-3	Sequence 3, Appli
C 17	33.8	6.7	2289	3 US-09-850-964-3	Sequence 3, Appli
C 18	33.6	6.6	1505	2 US-09-270-767-11623	Sequence 1299, Ap
C 19	33.2	6.5	567	4 US-09-605-703B-1299	Sequence 1299, Ap
C 20	33	6.5	336	2 US-07-14-220-4	Sequence 4, Appli
C 21	33	6.5	336	2 US-07-812-421-4	Sequence 4, Appli
C 22	32.6	6.4	700	3 US-09-731-271-1138	Sequence 1138, Ap
C 23	32.4	6.4	2689	2 US-08-465-795-2	Sequence 2, Appli
C 24	32.4	6.4	5589	2 US-08-465-795-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
 US-07-814-220-3/C

; Sequence 3, Application US/07814220
 ; Patent No. 5925540
 ; GENERAL INFORMATION:
 ; APPLICANT: Caceci, Thomas B.
 ; ADDRESS: 10000 N. University,
 ; CITY: Reston
 ; STATE: VA
 ; ZIP: 20191
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: WHITHAM, CURTIS & WHITHAM
 ; STREET: Reston Int'l. Center, 11800 Sunrise Valley Dr.,
 ; CITY: Reston
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 20191
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/814,220
 ; FILING DATE: 23-DEC-1991
 ; CLASSIFICATION: 435
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/588,437
 ; FILING DATE: 25-SEP-1990
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Whitham, Michael E.
 ; REGISTRATION NUMBER: 32,635
 ; REFERENCE DOCKET NUMBER: CIT.016
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 703-391-2510
 ; TELEFAX: 703-391-9035
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 336 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: CDS

age 2

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OM nucleic - nucleic search, using sw model

Run on: February 20, 2006, 11:17:34 ; Search time 613.737 Seconds
(without alignments)

6831.225 Million cell updates/sec

Title: US-10-785-981-5

Perfect score: 507

Sequence: tataagaaccgttttcagccgag 507

Scoring table: IDENTITY_NUC Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0\$ Maximum Match 100\$

Listing first 45 summaries

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; Sequence 5, Application US/10785981
; Publication No. US20050112597A1
; GENERAL INFORMATION:
; APPLICANT: CHULWOOK, KIM
; TITLE OF INVENTION: SCREENING EXPRESSION PROFILE OF GROWTH SPECIFIC GENES IN SWINE
; TITLE OF INVENTION: AND FUNCTIONAL CDNA CHIP PREPARED BY USING THE SAME
; FILE REFERENCE: 3884-0120P
; CURRENT APPLICATION NUMBER: US/10/785, 981
; CURRENT FILING DATE: 2004-06-26
; PRIORITY APPLICATION NUMBER: KR 2003-83653
; PRIORITY FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 507
; TYPE: DNA
; ORGANISM: Kagoshima Berkshire

US-10-785-981-5

Query Match 100.0%; Score 507; DB 9; Length 507;
Best Local Similarity 100.0%; Pred. No. 2.5e-161;
Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TATATAAGCGGATCAGTAGCTGGCTGACCAAGAGGGCCAAACAAAGGCCAACCT 60
Db 1 TATATAAGCGGATCAGTAGCTGGCTGACCAAGAGGGCCAAACAAAGGCCAACCT 60

Qy 61 AGGAGGTATAATAAGTTAGGCTGGCTGACATACCTACCGAAAGCGCG 120
Db 61 AGGAGGTATAATAAGTTAGGCTGGCTGACATACCTACCGAAAGCGCG 120

Qy 121 GGACAACTAGGGCTCGGCATAGCATTCCTTCTGGTCGATGTTGCGCTGCAG 180
Db 121 GGACAACTAGGGCTCGGCATAGCATTCCTTCTGGTCGATGTTGCGCTGCAG 180

Qy 181 TTATAGGGCTGCCAACCCCATACACCTTACAGCCACTTATTAGTTACATCAGGA 240
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Qy 241 GGCTCTGTACCAACCCTAAGCAGTGGCAAGTGTGGCTGCCTTGCGCTGCAG 300
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Result No. Score Query Match Length DB ID Description

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1 507 100.0 507 9 US-10-785-981-5 Sequence 5, Appli

2 507 100.0 507 9 US-10-785-981-5 Sequence 5, Appli

3 507 100.0 507 9 US-10-785-981-5 Sequence 5, Appli

4 123.2 24.3 505 7 US-10-424-599-13445 Sequence 881.82, A

5 61 12.0 523 7 US-10-424-599-13445 Sequence 79262, A

C 6 48.4 9.5 520 5 US-10-184-644-332 Sequence 332, App

C 7 48.4 9.5 520 5 US-10-184-634-332 Sequence 332, App

C 8 39.8 7.9 2852 10 US-11-097-143-1178 Sequence 1178, Ap

C 9 39.8 7.9 5023 10 US-11-097-143-1177 Sequence 1177, Ap

C 10 39.6 7.8 5059 7 US-10-424-599-13445 Sequence 13445, Ap

C 11 39.6 7.8 5643 6 US-10-012-952A-43 Sequence 43, Appli

C 12 38.6 7.6 3234 8 US-10-425-115-172916 Sequence 172916,

C 13 38 7.5 480 8 US-10-425-115-167155 Sequence 167155,

C 14 38 7.5 675 7 US-10-437-963-1319 Sequence 1319, Ap

C 15 37.2 7.3 2712 7 US-10-282-122A-24663 Sequence 24663, A

C 16 36.6 7.2 610 7 US-10-437-963-168546 Sequence 68546, A

C 17 36.6 7.2 1888 7 US-10-437-963-73429 Sequence 73429, A

C 18 36 7.1 728 7 US-10-398-221-1694 Sequence 1694, Ap

C 19 36 7.1 1296 7 US-10-398-221-610 Sequence 610, App

C 20 36 7.1 1311 7 US-10-398-221-613 Sequence 613, App

C 21 36 7.1 2034 7 US-10-398-221-3554 Sequence 3554, App

C 22 36 7.1 319630 7 US-10-398-221-7 Sequence 7, Appli

C 23 36 7.1 3011208 7 US-10-398-221-2058 Sequence 2058, Ap

§ SUMMARIES

Copyright GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 20, 2006, 11:27:30 ; Search time 387.381 Seconds
(without alignments)

Title: US-10-785-981-5
Perfect score: 507
Sequence: 1 tataatagaaccgaatcacgt.....tctgtcggtttcagccgacg 507

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Searched: 7204323 seqs, 1061406715 residues

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Post-processing: Minimum Match 0\$
Maximum Match 100%

Listing first 45 summaries

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 3: /cn2_6/podata/2/pubna/US07_NEW_PUB_seq:
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34.8	6.9	3990	12	US-11-052-554A-520 Sequence 520, App
2	32.2	6.4	2539	12	US-11-136-527-2523 Sequence 2523, App
3	32	6.3	523	6	US-09-925-065A-240456 Sequence 240456,
4	32	6.3	617	6	US-09-925-065A-461295 Sequence 461295,
5	32	6.3	993	12	US-11-128-061-930 Sequence 930, App
c 6	32	6.3	993	12	US-11-128-049-930 Sequence 930, App
c 7	32	6.3	1512	6	US-09-925-065A-62278 Sequence 62278, A
c 8	32	6.3	2223	8	US-10-467-657-6265 Sequence 6265, AP
c 9	32	6.3	2539	12	US-11-136-527-215 Sequence 215, App
c 10	31.8	6.3	2479	12	US-11-136-527-3303 Sequence 3303, App
c 11	31.4	6.2	476	6	US-09-925-065A-472363 Sequence 472363,
c 12	31.4	6.2	1090	6	US-09-925-065A-680565 Sequence 680565,
c 13	31.2	6.2	619	6	US-09-925-065A-874562 Sequence 874562,
c 14	31.2	6.2	978	8	US-10-793-626-3295 Sequence 3295, AP
c 15	31.2	6.2	2993	8	US-10-793-626-4155 Sequence 4155, AP
c 16	31.2	6.2	3585	8	US-10-793-626-3521 Sequence 3521, AP
c 17	31	6.1	255	8	US-10-909-125-1963 Sequence 1963, AP
c 18	31	6.1	889	12	US-11-136-527-3737 Sequence 3737, AP
c 19	31	6.1	889	12	US-11-136-527-4469 Sequence 4469, AP
c 20	31	6.1	2183	9	US-11-072-512-1064 Sequence 1064, AP

ALIGNMENTS

RESULT 1
US-11-052-554A-520
; Sequence 520, Application US/11052554A
; Publication No. US20050288866A1
; GENERAL INFORMATION:
; APPLICANT: Sachdeva, et al.
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE PROTEINS OF THERAPEUTIC POTENTIAL
; FILE REFERENCE: 30853/40359A
; CURRENT APPLICATION NUMBER: US/11/052,554A
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 60/589,227
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004
; PRIOR FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 763
; SEQ ID NO 520
; LENGTH: 3990
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis H37RV
; US-11-052-554A-520

Qy 358 CGGGGACTAGACAACGGTGTGGAGCGTAAGCGCTATGGTAGGAGTCGGCGACCG 417 ; SOFTWARE: FastSEQ for Windows Version 4.0
 Db 3288 AGGCCGAAAGGGCGCAGAGGGCAACGCCGCAAGGGCATCGGGGAA 3347 ; SEQ ID NO: 240456
 ; LENGTH: 523 ;
 ; TYPE: DNA ;
 ; ORGANISM: Homo sapiens ;
 US-09-925-065A-240456

Query Match 6.3%; Score 32; DB 6; Length 523;
 Best Local Similarity 48.9%; Pred. No. 3.8; ;
 Matches 86; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

Qy 418 CCGTGTAGCCAGCTTACTATGTTAGTTTCAAGAACCCCTGCCATAACCCCTGTTTC 477
 Db 3348 CGTGGGACCGGGGACACGGGACACGGGACACGGGAACTGGCAACGGCCAGGGCA 3407

Query Match 6.3%; Score 32; DB 6; Length 523;
 Best Local Similarity 48.9%; Pred. No. 3.8; ;
 Matches 86; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

Qy 44 CCAAACAGGGCAACCTAGGGTTATAAAATGGTATAAGCCATCTGGCGACACATAC 103
 Db 286 CAATTCCATGGTGAAGCTGAGGTTGAAAGCTGTGCGCTPATGCTGCAGTCAAATAAG 345

RESULT 2
 ; Sequence 2523, Application US/11136527
 ; Publication No. US20050287570A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wyeth
 ; ATTORNEY: Mounts, William M.
 ; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
 ; FILE REFERENCE: 031836-041000 (AM10.086)
 ; CURRENT FILING DATE: 2005-05-25
 ; PRIORITY APPLICATION NUMBER: US/11/136,527
 ; CURRENT FILING DATE: 2005-05-25
 ; PRIORITY FILING DATE: 2005-05-26
 ; NUMBER OF SEQ ID NOS: 362330
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO: 2523
 ; LENGTH: 2539
 ; TYPE: DNA
 ; ORGANISM: Rattus norvegicus
 US-11-136 527-2523

Query Match 6.4%; Score 32.2; DB 12; Length 2539;
 Best Local Similarity 48.6%; Pred. No. 4.7; ;
 Matches 85; Conservative 1; Mismatches 89; Indels 0; Gaps 0;

Qy 326 TTCCCCGATAGCCGCGCTTTTACACCAATCGGGACTAGACCCCTGGTGGCAC 385
 Db 431 TCCCCTAACGACGCCCTCGGGACCCCTGCTGAGCCCTCCGAGCTCAGAGCAC 490

Query Match 6.3%; Score 32; DB 6; Length 523;
 Best Local Similarity 48.9%; Pred. No. 3.9; ;
 Matches 86; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

Qy 386 GTAAGCTTATGGTAGCTGCTGAGCTGGCGGACGCCCTGTAACCTGTTAGT 445
 Db 491 AGCAGTAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 550

Query Match 6.3%; Score 32; DB 6; Length 523;
 Best Local Similarity 48.9%; Pred. No. 3.9; ;
 Matches 86; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

Qy 446 TTCAAGAACACCCTGGCAATACCCGGTTCCTRACTGTCGGTTCA 500
 Db 551 CCCTGCTCAAGCTGCCAACTCCAGGCCAGSTTGTCACTCCMGTGTTGCA 605

RESULT 3
 ; Sequence 240456, Application US/09925065A
 ; Publication No. US20040181048A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
 ; FILE REFERENCE: 108827-135
 ; CURRENT FILING DATE: 2001-08-08
 ; PRIORITY APPLICATION NUMBER: US/09/925, 065A
 ; CURRENT FILING DATE: 2000-10-24
 ; PRIORITY APPLICATION NUMBER: US 60/243, 096
 ; PRIORITY FILING DATE: 2000-11-20
 ; PRIORITY APPLICATION NUMBER: US 60/243, 096
 ; PRIORITY FILING DATE: 2000-10-24
 ; PRIORITY APPLICATION NUMBER: US 60/243, 096
 ; PRIORITY FILING DATE: 2000-11-20
 ; PRIORITY APPLICATION NUMBER: US 60/243, 096
 ; PRIORITY FILING DATE: 2000-11-30
 ; PRIORITY APPLICATION NUMBER: US 60/250, 092
 ; PRIORITY FILING DATE: 2000-11-30
 ; PRIORITY APPLICATION NUMBER: US 60/261, 766
 ; PRIORITY FILING DATE: 2001-01-16
 ; PRIORITY APPLICATION NUMBER: US 60/289, 846
 ; PRIORITY FILING DATE: 2001-05-09
 ; NUMBER OF SEQ ID NOS: 957086
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 461295
 ; LENGTH: 617
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-925-065A-461295

Query Match 6.3%; Score 32; DB 6; Length 617;
 Best Local Similarity 48.9%; Pred. No. 3.9; ;
 Matches 86; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

Qy 44 CCAAACAGGGCAACCTAGGGTTATAAAATGGTATAAGCCATCTGGCGACACATAC 103
 Db 10 CAAATCCATGGTGAAGCTGAGCTGAGGCTCCCTPATGCTGCAGTCAAATAAG 69

Query Match 6.3%; Score 32; DB 6; Length 523;
 Best Local Similarity 48.9%; Pred. No. 3.9; ;
 Matches 86; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

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 Db 70 CAGCTAAGAGAGGGCTGAGGAAACCTTGTGCAACGGCCATACACCTTACCCAGCA 219

Query Match 6.3%; Score 32; DB 6; Length 523;
 Best Local Similarity 48.9%; Pred. No. 3.9; ;
 Matches 86; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

Qy 164 GATGTGGGGCTGAGGAAACCTTGTGCAACGGCCATACACCTTACCCAGCA 219
 Db 130 CCAGCTCAGATAACTCTGTTAAAGGTTGTCAGAACATTGCGAGCA 185

RESULT 5
 ; Sequence 240456, Application US/09925065A
 ; Publication No. US20040181048A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
 ; FILE REFERENCE: 108827-135
 ; CURRENT FILING DATE: 2001-01-16
 ; PRIORITY APPLICATION NUMBER: US 60/289, 846
 ; PRIORITY FILING DATE: 2001-05-09
 ; PRIORITY APPLICATION NUMBER: US 60/289, 846
 ; PRIORITY FILING DATE: 2000-11-30
 ; PRIORITY APPLICATION NUMBER: US 60/250, 092
 ; PRIORITY FILING DATE: 2000-11-20
 ; PRIORITY APPLICATION NUMBER: US 60/243, 096
 ; PRIORITY FILING DATE: 2000-10-24
 ; PRIORITY APPLICATION NUMBER: US 60/243, 096
 ; PRIORITY FILING DATE: 2000-10-24
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